

- 699.3 Best-BlastP=> >nrrprot 59% Identities = 157/374 (41%), Positives = 226/374 (60%), Gaps = 4/374 (1%) ref|ZP_00089161.1| COG0607: Rhodanese-related sulfurtransferase [Azotobacter vinelandii] Length = 377
- 7.1 Best-BlastP=> >nrrprot 43% Identities = 394/1345 (29%), Positives = 596/1345 (44%), Gaps = 225/1345 (16%) ref|NP_907747.1| hypothetical protein WS1613 [Wolonia succinogenes] emb|CAE10647.1| hypothetical protein [Wolonia succinogenes] Length = 1409
- 701.2 Best-BlastP=> >nrrprot 62% Identities = 231/482 (47%), Positives = 307/482 (63%), Gaps = 6/482 (1%) ref|NP_819376.1| phosphomethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Coxiella burnetii RSA 493] gb|AAO89890.1| phosphomethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Coxiella burnetii RSA 493] Length = 479
- 702.2 Best-BlastP=> >nrrprot 73% Identities = 153/259 (59%), Positives = 193/259 (74%) ref|ZP_00067659.1| COG2022: Uncharacterized enzyme of thiazole biosynthesis [Microbulbifer degradans 2-40] Length = 269
- 704.4 Best-BlastP=> >nrrprot No Hits found
- 705.1 Best-BlastP=> >nrrprot 60% Identities = 179/427 (41%), Positives = 263/427 (61%), Gaps = 17/427 (3%) ref|NP_691145.1| hydroxymethylglutaryl-CoA reductase [Oceanobacillus iheyensis HTE831] dbj|BAC12180.1| hydroxymethylglutaryl-CoA reductase [Oceanobacillus iheyensis HTE831] Length = 429
- 706.2 Best-BlastP=> >nrrprot 27% Identities = 40/115 (34%), Positives = 49/115 (42%), Gaps = 1/115 (0%) pir|S75426 hypothetical protein c05009 - Sulfolobus solfataricus emb|CAA69540.1| orf c05009 [Sulfolobus solfataricus] Length = 115
- 707.2 Best-BlastP=> >nrrprot 57% Identities = 141/338 (41%), Positives = 196/338 (57%), Gaps = 4/338 (1%) ref|ZP_00072976.1| COG1304: L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases [Trichodesmium erythraeum IMS101] Length = 345
- 709.1 Best-BlastP=> >nrrprot No Hits found
- 711.2 Best-BlastP=> >nrrprot 74% Identities = 396/663 (59%), Positives = 497/663 (74%), Gaps = 2/663 (0%) ref|NP_249239.1| transketolase [Pseudomonas aeruginosa PA01] pir|B83577 transketolase PA0548 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG03937.1|AE004491_4 transketolase [Pseudomonas aeruginosa PAO1] Length = 665
- 712.2 Best-BlastP=> >nrrprot 79% Identities = 212/329 (64%), Positives = 263/329 (79%), Gaps = 5/329 (1%) ref|ZP_00033578.1| hypothetical protein [Burkholderia fungorum] Length = 336
- 713.2 Best-BlastP=> >nrrprot No Hits found
- 715.1 Best-BlastP=> >nrrprot No Hits found
- 716.1 Best-BlastP=> >nrrprot No Hits found
- 717.2 Best-BlastP=> >nrrprot No Hits found
- 719.4 Best-BlastP=> >nrrprot 75% Identities = 484/781 (61%), Positives = 592/781 (75%), Gaps = 24/781 (3%) ref|NP_901207.1| probable transcriptional accessory protein [Chromobacterium violaceum ATCC 12472] gb|AAQ59212.1| probable transcriptional accessory protein [Chromobacterium violaceum ATCC 12472] Length = 770
- 722.3 Best-BlastP=> >nrrprot 58% Identities = 79/215 (36%), Positives = 130/215 (60%), Gaps = 3/215 (1%) ref|NP_716217.1| thiopurine S-methyltransferase [Shewanella oneidensis MR-1] gb|AAN53662.1|AE015505_5 thiopurine S-methyltransferase [Shewanella oneidensis MR-1] Length = 218

- 723.3 Best-BlastP=> >nrprot 75% Identities = 353/611 (57%), Positives = 454/611 (74%), Gaps = 7/611 (1%) ref|NP_820767.1| glucosamine--fructose-6-phosphate aminotransferase, isomerizing [Coxiella burnetii RSA 493] gb|AAO91281.1| glucosamine--fructose-6-phosphate aminotransferase, isomerizing [Coxiella burnetii RSA 493] Length = 611
- 727.3 Best-BlastP=> >nrprot 82% Identities = 756/1070 (70%), Positives = 881/1070 (82%), Gaps = 5/1070 (0%) ref|NP_794254.1| carbamoyl-phosphate synthase, large subunit [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57949.1| carbamoyl-phosphate synthase, large subunit [Pseudomonas syringae pv. tomato str. DC3000] Length = 1073
- 728.2 Best-BlastP=> >nrprot 53% Identities = 49/111 (44%), Positives = 72/111 (64%) ref|NP_799407.1| CrcB protein [Vibrio parahaemolyticus RIMD 2210633] sp|Q87KE9|CrcB_VIBPA Protein crcB homolog dbj|BAC61291.1| CrcB protein [Vibrio parahaemolyticus] Length = 127
- 729.1 Best-BlastP=> >nrprot 73% Identities = 135/256 (52%), Positives = 190/256 (74%) ref|NP_252334.1| UDP-N-acetylglucosamine acyltransferase [Pseudomonas aeruginosa PA01] sp|Q9X6P4|LPXA_PSEAE Acyl-l-acyl-carrier-protein--UDP-N-acetylglucosamine O-acetyltransferase (UDP-N-acetylglucosamine acyltransferase) pir|D83190 UDP-N-acetylglucosamine acyltransferase PA3644 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAD30149.1|AF142597_1 hydroxydecanoyl-acyl carrier protein-dependent UDP-N-acetylglucosamine-3-O-acetyltransferase [Pseudomonas aeruginosa] gb|AAG07032.1|AE004784_5 UDP-N-acetylglucosamine acyltransferase [Pseudomonas aeruginosa PAO1] Length = 258
- 730.1 Best-BlastP=> >nrprot 68% Identities = 79/142 (55%), Positives = 104/142 (73%), Gaps = 1/142 (0%) ref|NP_873649.1| (3R)-hydroxymyristoyl-acyl carrier protein dehydratase [Haemophilus ducreyi 35000HP] gb|AAP96038.1| (3R)-hydroxymyristoyl-acyl carrier protein dehydratase [Haemophilus ducreyi 35000HP] Length = 154
- 731.2 Best-BlastP=> >nrprot 57% Identities = 132/334 (39%), Positives = 193/334 (57%) ref|NP_717250.1| UDP-3-O-(3-hydroxymyristoyl) glucosamine n-acyltransferase [Shewanella oneidensis MR-1] gb|AAN54694.1|AE015609_13 UDP-3-O-(3-hydroxymyristoyl) glucosamine n-acyltransferase [Shewanella oneidensis MR-1] Length = 341
- 732.3 Best-BlastP=> >nrprot 53% Identities = 50/139 (35%), Positives = 89/139 (64%) ref|NP_819642.1| outer membrane protein OmpH, putative [Coxiella burnetii RSA 493] gb|AAO90156.1| outer membrane protein OmpH, putative [Coxiella burnetii RSA 493] Length = 165
- 737.1 Best-BlastP=> >nrprot 45% Identities = 101/299 (33%), Positives = 156/299 (52%), Gaps = 15/299 (5%) ref|NP_812239.1| ATP-dependent DNA helicase recG [Bacteroides thetaiotaomicron VPI-5482] gb|AAO78433.1| ATP-dependent DNA helicase recG [Bacteroides thetaiotaomicron VPI-5482] Length = 485
- 738.2 Best-BlastP=> >nrprot 46% Identities = 48/153 (31%), Positives = 81/153 (52%), Gaps = 2/153 (1%) ref|NP_617319.1| ATP-dependent DNA helicase [Methanosarcina acetivorans str. C2A] gb|AAM05799.1| ATP-dependent DNA helicase [Methanosarcina acetivorans str. C2A] Length = 514
- 739.4 Best-BlastP=> >nrprot 69% Identities = 146/295 (49%), Positives = 202/295 (68%), Gaps = 10/295 (3%) ref|NP_052845.1| hypothetical protein [Coxiella burnetii] ref|NP_819051.1| parB protein, putative [Coxiella burnetii RSA 493] gb|AAD33477.1|AF131076_3 hypothetical protein [Coxiella burnetii] gb|AAO91611.1| parB protein, putative [Coxiella burnetii RSA 493] Length = 289
- 740.2 Best-BlastP=> >nrprot 81% Identities = 72/114 (63%), Positives = 93/114 (81%) ref|NP_772410.1| blt5770 [Bradyrhizobium japonicum] dbj|BAC51035.1| blt5770 [Bradyrhizobium japonicum USDA 110] Length = 118
- 741.2 Best-BlastP=> >nrprot No Hits found

- 742.3 Best-BlastP=> >nrprot 76% Identities = 280/467 (59%), Positives = 357/467 (76%), Gaps = 3/467 (0%) ref|NP_820336.1| amino acid antiporter [Coxiella burnetii RSA 493] gb|AAO90850.1| amino acid antiporter [Coxiella burnetii RSA 493] Length = 474
- 743.3 Best-BlastP=> >nrprot 94% Identities = 124/131 (94%), Positives = 125/131 (95%) gb|AAM00634.1| unknown [Legionella pneumophila] Length = 131
- 744.3 Best-BlastP=> >nrprot 97% Identities = 163/168 (97%), Positives = 164/168 (97%) gb|AAM00635.1| putative cadmium efflux ATPase [Legionella pneumophila] Length = 635
- 747.3 Best-BlastP=> >nrprot 99% Identities = 723/729 (99%), Positives = 725/729 (99%) gb|AAM00636.1| unknown [Legionella pneumophila] Length = 729
- 748.3 Best-BlastP=> >nrprot 30% Identities = 99/321 (30%), Positives = 137/321 (42%), Gaps = 72/321 (22%) ref|ZP_00129242.1| COG2821: Membrane-bound lytic murein transglycosylase [Desulfovibrio desulfuricans G20] Length = 442
- 749.1 Best-BlastP=> >nrprot No Hits found
- 750.2 Best-BlastP=> >nrprot No Hits found
- 751.2 Best-BlastP=> >nrprot No Hits found
- 752.2 Best-BlastP=> >nrprot No Hits found
- 753.2 Best-BlastP=> >nrprot 51% Identities = 92/311 (29%), Positives = 164/311 (52%), Gaps = 28/311 (9%) ref|NP_782216.1| conserved protein [Clostridium tetani E88] gb|AAO36153.1| conserved protein [Clostridium tetani E88] Length = 307
- 754.2 Best-BlastP=> >nrprot 62% Identities = 160/323 (49%), Positives = 209/323 (64%), Gaps = 6/323 (1%) ref|ZP_00107451.1| COG0667: Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) [Nostoc punctiforme] Length = 326
- 755.3 Best-BlastP=> >nrprot 46% Identities = 72/227 (31%), Positives = 126/227 (55%), Gaps = 12/227 (5%) ref|ZP_00065015.1| COG0062: Uncharacterized conserved protein [Microbulbifer degradans 2-40] Length = 500
- 757.1 Best-BlastP=> >nrprot 64% Identities = 95/203 (46%), Positives = 132/203 (65%), Gaps = 9/203 (4%) ref|NP_820677.1| 4Fe-4S binding domain protein [Coxiella burnetii RSA 493] gb|AAO91191.1| 4Fe-4S binding domain protein [Coxiella burnetii RSA 493] Length = 213
- 758.1 Best-BlastP=> >nrprot 82% Identities = 155/208 (74%), Positives = 174/208 (83%) ref|ZP_00122593.1| COG0177: Predicted EndoIII-related endonuclease [Haemophilus somnus 129PT] Length = 211
- 760.2 Best-BlastP=> >nrprot No Hits found
- 761.2 Best-BlastP=> >nrprot 22% Identities = 41/124 (33%), Positives = 70/124 (56%), Gaps = 8/124 (6%) ref|NP_656804.1| Acetyltransferase, Acetyltransferase (GNAT) family [Bacillus anthracis A2012] ref|NP_845271.1| acetyltransferase, GNAT family [Bacillus anthracis str. Ames] gb|AAP26757.1| acetyltransferase, GNAT family [Bacillus anthracis str. Ames] Length = 135
- 762.2 Best-BlastP=> >nrprot 56% Identities = 80/200 (40%), Positives = 123/200 (61%), Gaps = 1/200 (0%) ref|ZP_00086065.1| COG1280: Putative threonine efflux protein [Pseudomonas fluorescens PfO-1] Length = 209
- 764.1 Best-BlastP=> >nrprot 52% Identities = 53/167 (31%), Positives = 90/167 (53%), Gaps = 4/167 (2%) ref|NP_490158.1| probable acetyltransferase [Nostoc sp. PCC 7120] pir|AD2484 hypothetical protein alr7052 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha dbj|BAB78136.1| ORF_ID:alr7052~probable acetyltransferase [Nostoc sp. PCC 7120] Length = 169

- 765.1 Best-BlastP=> >nrprot 61% Identities = 99/234 (42%), Positives = 148/234 (63%), Gaps = 8/234 (3%) ref|NP_217318.1| hypothetical protein Rv2802c [Mycobacterium tuberculosis H37Rv] ref|NP_856471.1| HYPOTHETICAL ARGinine AND ALANINE RICH PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] pir|E70689 hypothetical protein Rv2802c - Mycobacterium tuberculosis (strain H37RV) emb|CAB03674.1| hypothetical protein Rv2802c [Mycobacterium tuberculosis H37Rv] emb|CAD95010.1| HYPOTHETICAL ARGinine AND ALANINE RICH PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] Length = 347
- 766.3 Best-BlastP=> >nrprot 36% Identities = 99/398 (24%), Positives = 173/398 (43%), Gaps = 71/398 (17%) ref|NP_845051.1| esterase, putative [Bacillus anthracis str. Ames] gb|AAP26537.1| esterase, putative [Bacillus anthracis str. Ames] Length = 382
- 767.3 Best-BlastP=> >nrprot 64% Identities = 206/430 (47%), Positives = 274/430 (63%), Gaps = 8/430 (1%) ref|NP_248707.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] pir|F83643 conserved hypothetical protein PA0017 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG03407.1|AE004441_8 conserved hypothetical protein [Pseudomonas aeruginosa PA01] Length = 434
- 769.2 Best-BlastP=> >nrprot 71% Identities = 167/311 (53%), Positives = 225/311 (72%), Gaps = 4/311 (1%) ref|ZP_00082909.1| COG0223: Methionyl-tRNA formyltransferase [Pseudomonas fluorescens PfO-1] Length = 319
- 77.1 Best-BlastP=> >nrprot No Hits found
- 770.3 Best-BlastP=> >nrprot 98% Identities = 157/161 (97%), Positives = 160/161 (99%) gb|AAD43221.1|AF111940_3 LspH precursor [Legionella pneumophila] Length = 161
- 771.4 Best-BlastP=> >nrprot 99% Identities = 140/140 (100%), Positives = 140/140 (100%) gb|AAD43220.1|AF111940_2 LspG precursor [Legionella pneumophila] gb|AAP69529.1| type II protein secretion LspG pseudopilin [Legionella pneumophila] Length = 140
- 772.4 Best-BlastP=> >nrprot 99% Identities = 393/399 (98%), Positives = 396/399 (99%) gb|AAK35047.2|AF330137_1 type II protein secretion LspF [Legionella pneumophila] Length = 399
- 774.3 Best-BlastP=> >nrprot 82% Identities = 325/469 (69%), Positives = 386/469 (82%) ref|NP_719933.1| glutamine synthetase, type I [Shewanella oneidensis MR-1] gb|AAN57377.1|AE015874_4 glutamine synthetase, type I [Shewanella oneidensis MR-1] Length = 469
- 775.2 Best-BlastP=> >nrprot 51% Identities = 62/171 (36%), Positives = 96/171 (56%), Gaps = 11/171 (6%) ref|NP_796499.1| hypothetical protein VP0120 [Vibrio parahaemolyticus RIMD 2210633] db|BAC58383.1| hypothetical protein [Vibrio parahaemolyticus] Length = 193
- 776.3 Best-BlastP=> >nrprot 99% Identities = 497/502 (99%), Positives = 500/502 (99%), Gaps = 1/502 (0%) gb|AAF34822.1|AF167992_2 IraB [Legionella pneumophila] Length = 501
- 778.2 Best-BlastP=> >nrprot 99% Identities = 272/272 (100%), Positives = 272/272 (100%) emb|CAB65217.1| hypothetical protein [Legionella pneumophila] gb|AAF34821.1|AF167992_1 small-molecule methyltransferase IraA [Legionella pneumophila] Length = 272
- 779.4 Best-BlastP=> >nrprot 99% Identities = 459/460 (99%), Positives = 460/460 (100%) emb|CAB65216.1| hypothetical protein [Legionella pneumophila] Length = 460
- 783.2 Best-BlastP=> >nrprot 62% Identities = 51/105 (48%), Positives = 75/105 (71%), Gaps = 1/105 (0%) ref|NP_359553.1| Conserved hypothetical protein [Streptococcus pneumoniae R6] pir|G98116 conserved hypothetical protein spr1962 [imported] - Streptococcus pneumoniae (strain R6) gb|AAL00764.1| Conserved hypothetical protein [Streptococcus pneumoniae R6] Length = 299

- 785.4 Best-BlastP=> >nrprot No Hits found
- 787.3 Best-BlastP=> >nrprot 68% Identities = 344/658 (52%), Positives = 452/658 (68%), Gaps = 23/658 (3%) ref|NP_718364.1| ribonuclease E [Shewanella oneidensis MR-1] gb|AAN55808.1|AE015717_9 ribonuclease E [Shewanella oneidensis MR-1] Length = 1088
- 789.4 Best-BlastP=> >nrprot 51% Identities = 25/77 (32%), Positives = 43/77 (55%) ref|NP_085189.1|IS10 orf [Shigella flexneri] ref|NP_858160.1| hypothetical protein [Shigella flexneri 2a] gb|AAK18345.1|AF348706_34 IS10 orf [Shigella flexneri] gb|AAL72480.1| hypothetical protein [Shigella flexneri 2a] Length = 407
- 79.1 CMCP6 ref|NP_759894.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_759900.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_759339.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_760021.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_760123.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_760329.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_760403.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_763327.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08317.1|AE016813_69 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08998.1|AE016798_158 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09421.1|AE016800_26 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09427.1|AE016800_32 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09466.1|AE016800_71 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09548.1|AE016800_153 Conserved hypothetical protein [Vibrio vulnificus CMCP6]
- 790.3 Best-BlastP=> >nrprot No Hits found
- 791.5 Best-BlastP=> >nrprot 98% Identities = 367/375 (97%), Positives = 372/375 (99%) gb|AAM00643.1| cyclopropane fatty acyl phospholipid synthase [Legionella pneumophila] Length = 375
- 793.2 Best-BlastP=> >nrprot No Hits found
- 794.2 Best-BlastP=> >nrprot No Hits found
- 795.2 Best-BlastP=> >nrprot 69% Identities = 134/260 (51%), Positives = 181/260 (69%), Gaps = 5/260 (1%) ref|NP_635864.1| indole-3-glycerol phosphate synthase [Xanthomonas campestris pv. campestris str. ATCC 33913] sp|Q8PD70|TRPC_XANCP Indole-3-glycerol phosphate synthase (IGPS) gb|AAM39788.1| indole-3-glycerol phosphate synthase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 265
- 796.2 Best-BlastP=> >nrprot 39% Identities = 60/227 (26%), Positives = 98/227 (43%), Gaps = 25/227 (11%) ref|NP_783943.1| adenylyl transferase (putative) [Lactobacillus plantarum WCFS1] emb|CAD62779.1| adenylyl transferase (putative) [Lactobacillus plantarum WCFS1] Length = 259
- 798.2 Best-BlastP=> >nrprot 60% Identities = 242/575 (42%), Positives = 364/575 (63%), Gaps = 8/575 (1%) ref|NP_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589
- 799.3 Best-BlastP=> >nrprot 50% Identities = 156/500 (31%), Positives = 249/500 (49%), Gaps = 60/500 (12%) ref|ZP_00112433.1| COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Nostoc punctiforme] Length = 544

- 80.3 Best-BlastP=> >nrprot 77% Identities = 34/42 (80%), Positives = 34/42 (80%) ref|NP_759472.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_759895.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_759901.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_760122.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_760328.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP_763326.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08316.1|AE016813_68 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08999.1|AE016798_159 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09422.1|AE016800_27 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09428.1|AE016800_33 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09649.1|AE016800_254 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 43
- 801.3 Best-BlastP=> >nrprot 61% Identities = 104/249 (41%), Positives = 152/249 (61%), Gaps = 3/249 (1%) ref|ZP_00032174.1| COG4787: Flagellar basal body rod protein [Burkholderia fungorum] Length = 461
- 802.3 Best-BlastP=> >nrprot 74% Identities = 158/261 (60%), Positives = 196/261 (75%) ref|NP_249773.1| flagellar basal-body rod protein FlgG [Pseudomonas aeruginosa PA01] ref|ZP_00138668.1| COG4786: Flagellar basal body rod protein [Pseudomonas aeruginosa UCBPP-PA14] pir|H83510 flagellar basal-body rod protein FlgG PA1082 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04471.1|AE004539_13 flagellar basal-body rod protein FlgG [Pseudomonas aeruginosa PAO1] Length = 261
- 803.3 Best-BlastP=> >nrprot 58% Identities = 84/223 (37%), Positives = 136/223 (60%), Gaps = 3/223 (1%) gb|AAN08643.1| FlgH [Aeromonas hydrophila] Length = 223
- 806.2 Best-BlastP=> >nrprot 41% Identities = 54/206 (26%), Positives = 102/206 (49%), Gaps = 11/206 (5%) sp|Q00924|HYUE_PSESN HYDANTOIN RACEMASE pir|B41895 hydantoin racemase HyuE - Pseudomonas sp gb|AAA25843.1| 5-substituted hydantoin racemase Length = 249
- 807.2 Best-BlastP=> >nrprot 46% Identities = 135/390 (34%), Positives = 205/390 (52%), Gaps = 14/390 (3%) ref|ZP_00090340.1| COG0402: Cytosine deaminase and related metal-dependent hydrolases [Azotobacter vinelandii] Length = 463
- 808.4 Best-BlastP=> >nrprot 20% Identities = 110/492 (22%), Positives = 193/492 (39%), Gaps = 57/492 (11%) ref|NP_213438.1| chromosome assembly protein homolog [Aquifex aeolicus] pir|B70356 chromosome assembly protein homolog - Aquifex aeolicus gb|AAC06839.1| chromosome assembly protein homolog [Aquifex aeolicus VF5] Length = 1156
- 81.3 Best-BlastP=> >nrprot 52% Identities = 20/40 (50%), Positives = 24/40 (60%) ref|NP_907600.1| hypothetical protein WS1440 [Wolinella succinogenes] emb|CAE10500.1| hypothetical protein [Wolinella succinogenes] Length = 42
- 813.2 Best-BlastP=> >nrprot 60% Identities = 178/412 (43%), Positives = 259/412 (62%), Gaps = 8/412 (1%) ref|NP_821038.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO91552.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 446
- 815.2 Best-BlastP=> >nrprot 75% Identities = 251/408 (61%), Positives = 306/408 (75%), Gaps = 7/408 (1%) ref|NP_671036.1| phosphopentomutase [Yersinia pestis KIM] gb|AAM87287.1|AE013977_6 phosphopentomutase [Yersinia pestis KIM] Length = 429
- 817.7 Best-BlastP=> >nrprot 21% Identities = 198/995 (19%), Positives = 410/995 (41%), Gaps = 142/995 (14%) dbj|BAA34954.1| myosin heavy chain [Dugesia japonica] Length = 1958

- 818.2 Best-BlastP=> >nrprot 42% Identities = 68/304 (22%), Positives = 122/304 (40%), Gaps = 28/304 (9%) ref|NP_866394.1| ATP synthase gamma subunit C-terminus homolog [Pirellula sp.] emb|CAD78175.1| ATP synthase gamma subunit C-terminus homolog [Pirellula sp.] Length = 306
- 819.2 Best-BlastP=> >nrprot 67% Identities = 217/484 (44%), Positives = 330/484 (68%), Gaps = 11/484 (2%) ref|NP_229412.1| ATP synthase F1, subunit alpha [Thermotoga maritima] pir|F72231| ATP synthase F1, subunit alpha - Thermotoga maritima (strain MSB8) gb|AAD36679.1|AE001805_4 ATP synthase F1, subunit alpha [Thermotoga maritima] Length = 503
- 82.2 Best-BlastP=> >nrprot 28% Identities = 23/33 (69%), Positives = 24/33 (72%) pir|A44803| pG1 protein - human (fragment) Length = 75
- 821.2 Best-BlastP=> >nrprot No Hits found
- 823.4 Best-BlastP=> >nrprot 68% Identities = 143/268 (53%), Positives = 184/268 (68%), Gaps = 5/268 (1%) ref|NP_820923.1| UDP-N-acetylglucosamine pyrophosphorylase [Coxiella burnetii] RSA 493 gb|AAO91437.1| UDP-N-acetylglucosamine pyrophosphorylase [Coxiella burnetii] RSA 493 Length = 455
- 825.4 Best-BlastP=> >nrprot 99% Identities = 407/413 (98%), Positives = 411/413 (99%) gb|AAM00639.1| aresenite efflux membrane component-like protein [Legionella pneumophila] Length = 413
- 829.2 Best-BlastP=> >nrprot 80% Identities = 373/541 (68%), Positives = 457/541 (84%) ref|NP_888942.1| putative sulfate transporter [Bordetella bronchiseptica] emb|CAE32896.1| putative sulfate transporter [Bordetella bronchiseptica] Length = 563
- 830.4 Best-BlastP=> >nrprot 45% Identities = 229/949 (24%), Positives = 392/949 (41%), Gaps = 162/949 (17%) ref|NP_819243.1| conserved hypothetical protein [Coxiella burnetii] RSA 493 gb|AAO89757.1| conserved hypothetical protein [Coxiella burnetii] RSA 493 Length = 929
- 832.3 Best-BlastP=> >nrprot 70% Identities = 186/321 (57%), Positives = 235/321 (73%), Gaps = 5/321 (1%) ref|NP_615542.1| porphobilinogen synthase [Methanosarcina acetivorans str. C2A] gb|AAM04022.1| porphobilinogen synthase [Methanosarcina acetivorans str. C2A] Length = 324
- 833.3 Best-BlastP=> >nrprot 33% Identities = 170/674 (25%), Positives = 264/674 (39%), Gaps = 134/674 (19%) ref|NP_798717.1| chitinase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60601.1| chitinase [Vibrio parahaemolyticus] Length = 848
- 835.2 Best-BlastP=> >nrprot 60% Identities = 355/836 (42%), Positives = 523/836 (62%), Gaps = 12/836 (1%) ref|NP_252348.1| protein-PII uridylyltransferase [Pseudomonas aeruginosa PAO1] sp|Q9Z9H0|GLND_PSEAE [Protein-PII] uridylyltransferase (PII uridylyl-transferase) (Uridyl removing enzyme) (UTase) pir|E83189| protein-PII uridylyltransferase PA3658 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07046.1|AE004785_10 protein-PII uridylyltransferase [Pseudomonas aeruginosa PAO1] Length = 900
- 837.2 Best-BlastP=> >nrprot 82% Identities = 185/255 (72%), Positives = 210/255 (82%), Gaps = 1/255 (0%) ref|NP_820377.1| methionine aminopeptidase, type I [Coxiella burnetii] RSA 493 gb|AAO90891.1| methionine aminopeptidase, type I [Coxiella burnetii] RSA 493 Length = 258
- 838.3 Best-BlastP=> >nrprot 80% Identities = 322/460 (70%), Positives = 372/460 (80%) ref|NP_710366.1| Fumarate hydratase [Leptospira interrogans serovar lai str. 56601] gb|AAN47384.1|AE011209_3 Fumarate hydratase [Leptospira interrogans serovar lai str. 56601] Length = 464

- 84.4 Best-BlastP=> >nrprot 59% Identities = 243/551 (44%), Positives = 334/551 (60%), Gaps = 49/551 (8%) ref|NP_819689.1| DNA polymerase III, gamma and tau subunits [Coxiella burnetii RSA 493] gb|AAO90203.1| DNA polymerase III, gamma and tau subunits [Coxiella burnetii RSA 493] Length = 509
- 840.2 Best-BlastP=> >nrprot 63% Identities = 124/242 (51%), Positives = 155/242 (64%) ref|NP_404551.1| conserved hypothetical protein [Yersinia pestis] ref|NP_670619.1| hypothetical protein [Yersinia pestis KIM] pir|AF0114 conserved hypothetical protein YPO0934 [imported] - Yersinia pestis (strain CO92) emb|CAC89777.1| conserved hypothetical protein [Yersinia pestis CO92] gb|AAM86870.1|AE013933_7 hypothetical protein [Yersinia pestis KIM] Length = 243
- 841.3 Best-BlastP=> >nrprot 78% Identities = 70/108 (64%), Positives = 86/108 (79%) ref|ZP_00023150.1| COG0526: Thiol-disulfide isomerase and thioredoxins [Ralstonia metalidurans] Length = 108
- 843.2 Best-BlastP=> >nrprot 99% Identities = 188/189 (99%), Positives = 189/189 (100%) emb|CAD90948.1| putative pyrimidine phosphoribosyl transferase [Legionella pneumophila] Length = 189
- 844.2 Best-BlastP=> >nrprot 70% Identities = 61/101 (60%), Positives = 77/101 (76%), Gaps = 2/101 (1%) ref|ZP_00068029.1| COG4517: Uncharacterized protein conserved in bacteria [Microbulifer degradans 2-40] Length = 189
- 845.4 Best-BlastP=> >nrprot 38% Identities = 54/212 (25%), Positives = 97/212 (45%), Gaps = 6/212 (2%) ref|NP_819358.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89872.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 243
- 847.4 Best-BlastP=> >nrprot 68% Identities = 562/1047 (53%), Positives = 719/1047 (68%), Gaps = 18/1047 (1%) ref|NP_639180.1| bifunctional PutA protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM43071.1| bifunctional PutA protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 1066
- 852.3 Best-BlastP=> >nrprot 58% Identities = 92/194 (47%), Positives = 116/194 (59%) ref|NP_642158.1| amidotransferase [Xanthomonas axonopodis pv. citri str. 306] gb|AAM36694.1| amidotransferase [Xanthomonas axonopodis pv. citri str. 306] Length = 200
- 853.1 Best-BlastP=> >nrprot 62% Identities = 99/239 (41%), Positives = 149/239 (62%), Gaps = 2/239 (0%) ref|NP_928857.1| phosphoribosylformimino-5-aminimidazole carboxamide ribotide isomerase [Photorhabdus luminescens subsp. laumondii emb|CAE13859.1| phosphoribosylformimino-5-aminimidazole carboxamide ribotide isomerase [Photorhabdus luminescens subsp. laumondii TTO1] Length = 245
- 854.3 Best-BlastP=> >nrprot 62% Identities = 97/179 (54%), Positives = 132/179 (73%), Gaps = 2/179 (1%) ref|NP_797522.1| imidazoleglycerol-phosphate synthase, cyclase subunit [Vibrio parahaemolyticus RIMD 2210633] sp|Q87QK6|HIS6_VIBPA Imidazole glycerol phosphate synthase subunit hisF (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (IGPS subunit hisF) dbj|BAC59406.1| imidazoleglycerol-phosphate synthase, cyclase subunit [Vibrio parahaemolyticus] Length = 257
- 856.2 Best-BlastP=> >nrprot No Hits found
- 857.2 Best-BlastP=> >nrprot 64% Identities = 349/779 (44%), Positives = 498/779 (63%), Gaps = 20/779 (2%) ref|NP_668468.1| putative penicillin-binding protein [Yersinia pestis KIM] gb|AAM84719.1|AE013717_1 putative penicillin-binding protein [Yersinia pestis KIM] Length = 845
- 858.2 Best-BlastP=> >nrprot 60% Identities = 71/157 (45%), Positives = 99/157 (63%) ref|ZP_00089699.1| COG1376: Uncharacterized protein conserved in bacteria [Azotobacter vinelandii] Length = 174

- 859.2 Best-BlastP=> >nrprot 69% Identities = 240/454 (52%), Positives = 324/454 (71%) ref|NP_820199.1| aldehyde dehydrogenase family protein [Coxiella burnetii RSA 493] gb|AAO90713.1| aldehyde dehydrogenase family protein [Coxiella burnetii RSA 493] Length = 455
- 860.2 Best-BlastP=> >nrprot 28% Identities = 112/372 (30%), Positives = 167/372 (44%), Gaps = 46/372 (12%) ref|XP_313257.1| ENSANGP00000010409 [Anopheles gambiae] gb|EAA08897.1| ENSANGP00000010409 [Anopheles gambiae str. PEST] Length = 2206
- 862.1 Best-BlastP=> >nrprot No Hits found
- 863.1 Best-BlastP=> >nrprot 72% Identities = 70/114 (61%), Positives = 90/114 (78%) ref|ZP_00092569.1| COG3293: Transposase and inactivated derivatives [Azotobacter vinelandii] Length = 249
- 864.1 Best-BlastP=> >nrprot 85% Identities = 70/95 (73%), Positives = 83/95 (87%) ref|NP_820693.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91207.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 96
- 865.2 Best-BlastP=> >nrprot 75% Identities = 227/379 (59%), Positives = 280/379 (73%), Gaps = 12/379 (3%) ref|NP_232020.1| carbamoyl-phosphate synthase, small subunit [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KPH8|CARA_VIBCH Carbamoyl-phosphate synthase small chain (Carbamoyl-phosphate synthetase glutamine chain) pir||E82083 carbamoyl-phosphate synthase, small chain VC2390 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95533.1| carbamoyl-phosphate synthase, small subunit [Vibrio cholerae O1 biovar eltor str. N16961] Length = 379
- 866.2 Best-BlastP=> >nrprot 99% Identities = 379/379 (100%), Positives = 379/379 (100%) sp|P50025|DNAJ_LEGPN Chaperone protein dnaJ gb|AAA80278.1| heat-shock protein Length = 379
- 869.2 Best-BlastP=> >nrprot No Hits found
- 870.3 Best-BlastP=> >nrprot 98% Identities = 355/360 (98%), Positives = 357/360 (99%) pir||T18333 icmK protein - Legionella pneumophila gb|AAC38189.1| DotJ [Legionella pneumophila] emb|CAA75330.1| icmK protein [Legionella pneumophila] Length = 360
- 872.2 Best-BlastP=> >nrprot 99% Identities = 212/212 (100%), Positives = 212/212 (100%) pir||T18332 icmL protein - Legionella pneumophila gb|AAC38190.1| DotI [Legionella pneumophila] emb|CAA75329.1| icmL protein [Legionella pneumophila] emb|CAD43145.1| DotI protein [Legionella pneumophila serogroup 6] Length = 212
- 873.2 Best-BlastP=> >nrprot 96% Identities = 91/94 (96%), Positives = 92/94 (97%) pir||T18331 icmM protein - Legionella pneumophila gb|AAC38191.1| DotJ [Legionella pneumophila] emb|CAA75328.1| icmM protein [Legionella pneumophila] Length = 94
- 874.2 Best-BlastP=> >nrprot 99% Identities = 187/189 (98%), Positives = 189/189 (100%) pir||T18330 lphA protein - Legionella pneumophila emb|CAA75327.1| LphA protein [Legionella pneumophila] Length = 189
- 875.5 Best-BlastP=> >nrprot 53% Identities = 133/408 (32%), Positives = 227/408 (55%), Gaps = 10/408 (2%) ref|NP_827016.1| putative integral membrane transport protein [Streptomyces avermitilis MA-4680] dbj|BAC73551.1| putative integral membrane transport protein [Streptomyces avermitilis MA-4680] Length = 490

- 876.1 Best-BlastP=> >nrprot 23% Identities = 23/67 (34%), Positives = 37/67 (55%), Gaps = 2/67 (2%) ref|NP_355599.1| AGR_C_4826p [Agrobacterium tumefaciens] ref|NP_53327.1| acetyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|G97678 hypothetical protein AGR_C_4826 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AE2903 acetyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK88384.1| AGR_C_4826p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL43643.1| acetyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 168
- 879.2 Best-BlastP=> >nrprot 60% Identities = 65/153 (42%), Positives = 94/153 (61%), Gaps = 10/153 (6%) ref|ZP_00090468.1| COG0582: Integrase [Azotobacter vinelandii] Length = 399
- 880.3 Best-BlastP=> >nrprot 60% Identities = 137/352 (38%), Positives = 215/352 (61%) ref|NP_819830.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90344.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 355
- 881.2 Best-BlastP=> >nrprot 61% Identities = 141/359 (39%), Positives = 221/359 (61%), Gaps = 7/359 (1%) ref|NP_819829.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90343.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 370
- 882.3 Best-BlastP=> >nrprot 63% Identities = 218/487 (44%), Positives = 308/487 (63%), Gaps = 12/487 (2%) ref|NP_439847.1| aminopeptidase A/[Haemophilus influenzae Rd] sp|P45334|AMPA_HAEIN Cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) pir|C64137 leucyl aminopeptidase (EC 3.4.11.1) A - Haemophilus influenzae (strain Rd KW20) gb|AAC23351.1| aminopeptidase A/[pepA] [Haemophilus influenzae Rd] Length = 491
- 884.3 Best-BlastP=> >nrprot 23% Identities = 48/193 (24%), Positives = 77/193 (39%), Gaps = 9/193 (4%) ref|NP_624872.1| hypothetical protein SCF73.06c [Streptomyces coelicolor A3(2)] emb|CAB57411.1| hypothetical protein SCF73.06c [Streptomyces coelicolor A3(2)] Length = 333
- 885.2 Best-BlastP=> >nrprot 38% Identities = 160/289 (55%), Positives = 204/289 (70%) ref|NP_386181.1| HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] emb|CAC46654.1| HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] Length = 299
- 886.3 Best-BlastP=> >nrprot 31% Identities = 50/153 (32%), Positives = 83/153 (54%), Gaps = 2/153 (1%) ref|NP_799124.1| shikimate kinase [Vibrio parahaemolyticus RIMD 2210633] sp|Q87L67|AROK_VIBPA Shikimate kinase (SK) db|BAC61008.1| shikimate kinase [Vibrio parahaemolyticus] Length = 172
- 887.4 Best-BlastP=> >nrprot 18% Identities = 82/315 (26%), Positives = 132/315 (41%), Gaps = 67/315 (21%) ref|NP_229450.1| alpha-amylase, putative [Thermotoga maritima] pir|G7227 hypothetical protein TM1650 - Thermotoga maritima (strain MSB8) gb|AAD36717.1|AE001807_8 alpha-amylase, putative [Thermotoga maritima] Length = 422
- 888.3 Best-BlastP=> >nrprot 73% Identities = 240/415 (57%), Positives = 303/415 (73%), Gaps = 2/415 (0%) ref|NP_794674.1| GTP-binding protein HflX [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58369.1| GTP-binding protein HflX [Pseudomonas syringae pv. tomato str. DC3000] Length = 433
- 889.1 Best-BlastP=> >nrprot 45% Identities = 45/128 (35%), Positives = 71/128 (55%), Gaps = 1/128 (0%) sp|P35160|RESA_BACSU Thiol-disulfide oxidoreductase resA Length = 179
- 891.3 Best-BlastP=> >nrprot 29% Identities = 84/420 (20%), Positives = 157/420 (37%), Gaps = 1/15/420 (27%) emb|CAC18568.1| phosphatidylcholine-hydrolyzing phospholipase C [Pseudomonas fluorescens] Length = 385

- 893.4 Best-BlastP=> >nrprot 67% Identities = 430/811 (53%), Positives = 561/811 (69%), Gaps = 6/811 (0%) dbj|BAA77891.1| Acyl-CoA dehydrogenase (EC 1.3.99.-) [Escherichia coli] Length = 840
- 894.3 Best-BlastP=> >nrprot No Hits found
- 895.3 Best-BlastP=> >nrprot 54% Identities = 102/300 (34%), Positives = 159/300 (53%), Gaps = 25/300 (8%) ref|ZP_00107238.1| COG0697: Permeases of the drug/metabolite transporter (DMT) superfamily [Nostoc punctiforme] Length = 369
- 897.2 Best-BlastP=> >nrprot 99% Identities = 764/764 (100%), Positives = 764/764 (100%) gb|AAAF05327.2| phosphoenolpyruvate-protein phosphotransferase PtsP [Legionella pneumophila] Length = 764
- 898.2 Best-BlastP=> >nrprot 57% Identities = 96/257 (37%), Positives = 156/257 (60%), Gaps = 1/257 (0%) ref|ZP_00130066.1| COG0730: Predicted permeases [Desulfovibrio desulfuricans G20] Length = 265
- 899.3 Best-BlastP=> >nrprot 77% Identities = 163/257 (63%), Positives = 200/257 (77%), Gaps = 1/257 (0%) ref|NP_820532.1| prolipoprotein diacylglycerol transferase [Coxiella burnetii RSA 493] gb|AAO91046.1| prolipoprotein diacylglycerol transferase [Coxiella burnetii RSA 493] Length = 261
- 9.1 Best-BlastP=> >nrprot 44% Identities = 57/140 (40%), Positives = 75/140 (53%), Gaps = 4/140 (2%) dbj|BAC94688.1| hypothetical protein [Vibrio vulnificus YJ016] Length = 343
- 901.2 Best-BlastP=> >nrprot No Hits found
- 903.2 Best-BlastP=> >nrprot No Hits found
- 905.2
- Best-BlastP=> >nrprot 78% Identities = 176/285 (61%), Positives = 225/285 (78%), Gaps = 2/285 (0%) ref|NP_773784.1| oxidoreductase [Bradyrhizobium japonicum] dbj|BAC52409.1| oxidoreductase [Bradyrhizobium japonicum USDA 110] Length = 308
- 907.4 Best-BlastP=> >nrprot 81% Identities = 571/879 (64%), Positives = 727/879 (82%), Gaps = 2/879 (0%) ref|ZP_00091354.1| COG2609: Pyruvate dehydrogenase complex, dehydrogenase (E1) component [Azotobacter vinelandii] Length = 893
- 908.4
- Best-BlastP=> >nrprot 69% Identities = 273/562 (48%), Positives = 378/562 (67%), Gaps = 26/562 (4%) ref|NP_716062.1| pyruvate dehydrogenase complex, E2 component, dihydrolipoamide acetyltransferase [Shewanella oneidensis MR-1] gb|AAN53507.1| AE015490_8 pyruvate dehydrogenase complex, E2 component, dihydrolipoamide acetyltransferase [Shewanella oneidensis MR-1] Length = 677
- 909.2 Best-BlastP=> >nrprot 54% Identities = 107/278 (38%), Positives = 156/278 (56%) ref|NP_820642.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91156.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 294
- 910.4 Best-BlastP=> >nrprot 78% Identities = 476/739 (64%), Positives = 590/739 (79%) ref|NP_253651.1| topoisomerase IV subunit A [Pseudomonas aeruginosa PAO1] pir|G83025 topoisomerase IV subunit A PA4964 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08349.1| AE004909_5 topoisomerase IV subunit A [Pseudomonas aeruginosa PAO1] Length = 754
- 914.3 Best-BlastP=> >nrprot 70% Identities = 338/573 (58%), Positives = 411/573 (71%), Gaps = 6/573 (1%) gb|AAL27383.1| AF426171_14 putative ABC transporter ElsE [Yersinia pestis] Length = 580

- 915.3 Best-BlastP=> >nrprot 64% Identities = 132/332 (39%), Positives = 183/332 (55%), Gaps = 54/332 (16%) ref|NP_455356.1| HlyD-family secretion protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_805830.1| HlyD-family secretion protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] sp|Q8Z879|YBHG_SALTI Hypothetical UPF0194 membrane protein ybhG pir|AG0599 HlyD-family secretion protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) emb|CAD05265.1| HlyD-family secretion protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO69690.1| HlyD-family secretion protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 331
- 916.3 Best-BlastP=> >nrprot 69% Identities = 162/336 (48%), Positives = 232/336 (69%), Gaps = 11/336 (3%) ref|NP_819097.1| ferrochelataase [Coxiella burnetii RSA 493] gb|AAO89611.1| ferrochelataase [Coxiella burnetii RSA 493] Length = 343
- 917.3 Best-BlastP=> >nrprot 65% Identities = 43/71 (60%), Positives = 51/71 (71%) ref|NP_404959.1| cold shock-like protein [Yersinia pestis] pir|AH0166 cold shock-like protein [imported] - Yersinia pestis (strain CO92) emb|CAC90195.1| cold shock-like protein [Yersinia pestis CO92] Length = 87
- 918.3 Best-BlastP=> >nrprot No Hits found
- 919.1 Best-BlastP=> >nrprot 62% Identities = 51/125 (40%), Positives = 86/125 (68%), Gaps = 1/125 (0%) ref|NP_249650.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|A83524 hypothetical protein PA0959 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04348.1|AE004530_1 hypothetical protein PA0959 [Pseudomonas aeruginosa PAO1] Length = 209
- 920.2 Best-BlastP=> >nrprot 43% Identities = 28/116 (24%), Positives = 52/116 (44%), Gaps = 4/116 (3%) ref|ZP_00082077.1| hypothetical protein [Geobacter metallireducens] Length = 130
- 921.3 Best-BlastP=> >nrprot 71% Identities = 107/194 (55%), Positives = 141/194 (72%), Gaps = 1/194 (0%) ref|NP_760875.1| Recombinational DNA repair protein [Vibrio vulnificus CMCP6] sp|Q8DB22|RECR_VIBVU Recombination protein recR gb|AAO10402.1|AE016803_189 Recombinational DNA repair protein [Vibrio vulnificus CMCP6] dbj|BAC95173.1| Recombinational DNA repair protein [Vibrio vulnificus YJ016] Length = 200
- 922.2 Best-BlastP=> >nrprot 54% Identities = 101/244 (41%), Positives = 150/244 (61%), Gaps = 10/244 (4%) ref|NP_232123.1| hypothetical protein VC2494 [Vibrio cholerae O1 biovar eltor str. N16961] pir|A82069 hypothetical protein VC2494 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95636.1| hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 263
- 923.3 Best-BlastP=> >nrprot 26% Identities = 104/453 (22%), Positives = 180/453 (39%), Gaps = 103/453 (22%) ref|NP_126866.1| hypothetical protein [Pyrococcus abyssi] pir|C75099 hypothetical protein PAB0793 - Pyrococcus abyssi (strain Orsay) emb|CAB50096.1| Sulfatase [Pyrococcus abyssi] Length = 479
- 925.3 Best-BlastP=> >nrprot 63% Identities = 282/620 (45%), Positives = 401/620 (64%), Gaps = 9/620 (1%) ref|NP_246321.1| SpeA [Pasteurella multocida] gb|AAK03466.1| SpeA [Pasteurella multocida] Length = 644
- 926.4 Best-BlastP=> >nrprot 55% Identities = 85/232 (36%), Positives = 130/232 (56%), Gaps = 1/232 (0%) ref|NP_743997.1| glutamine amidotransferase, class I [Pseudomonas putida KT2440] gb|AAN67461.1|AE016373_3 glutamine amidotransferase, class I [Pseudomonas putida KT2440] Length = 244
- 928.1 Best-BlastP=> >nrprot 72% Identities = 217/380 (57%), Positives = 279/380 (73%) ref|NP_386317.1| PUTATIVE ALCOHOL DEHYDROGENASE PROTEIN [Sinorhizobium meliloti] emb|CAC46790.1| PUTATIVE ALCOHOL DEHYDROGENASE PROTEIN [Sinorhizobium meliloti] Length = 381

- 929.2 Best-BlastP=> >nrprot 72% Identities = 255/464 (54%), Positives = 339/464 (73%), Gaps = 3/464 (0%) ref|NP_104264.1| dehydrogenase, (succinatesemialdehyde dehydrogenase, aldehyde dehydrogenase, aldehyde dehydrogenase) [Mesorhizobium loti] dbj|BAB50050.1| dehydrogenase; succinatesemialdehyde dehydrogenase; aldehyde dehydrogenase [Mesorhizobium loti] Length = 462
- 930.3 Best-BlastP=> >nrprot 67% Identities = 226/441 (51%), Positives = 309/441 (70%), Gaps = 3/441 (0%) ref|NP_220602.1| CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (cydA) [Rickettsia prowazekii] pir|H71732 cytochrome D ubiquinol oxidase chain I (cydA) RP216 - Rickettsia prowazekii emb|CAA14679.1| CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (cydA) [Rickettsia prowazekii] Length = 453
- 932.1 Best-BlastP=> >nrprot 69% Identities = 157/331 (47%), Positives = 229/331 (69%), Gaps = 3/331 (0%) ref|NP_794398.1| cyanide-insensitive terminal oxidase CioB [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58093.1| cyanide-insensitive terminal oxidase CioB [Pseudomonas syringae pv. tomato str. DC3000] Length = 335
- 935.2 Best-BlastP=> >nrprot 50% Identities = 81/260 (31%), Positives = 132/260 (50%), Gaps = 6/260 (2%) ref|NP_532654.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AD2819 conserved hypothetical protein Atu1975 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAL42970.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 262
- 936.3 Best-BlastP=> >nrprot 35% Identities = 38/156 (24%), Positives = 65/156 (41%), Gaps = 22/156 (14%) ref|NP_718932.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56376.1| AE015774_11 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 190
- 937.3 Best-BlastP=> >nrprot 67% Identities = 237/470 (50%), Positives = 320/470 (68%), Gaps = 8/470 (1%) ref|NP_820223.1| sensor histidine kinase [Coxiella burnetii RSA 493] gb|AAO90737.1| sensor histidine kinase [Coxiella burnetii RSA 493] Length = 478
- 938.3 Best-BlastP=> >nrprot 6% Identities = 22/49 (44%), Positives = 36/49 (73%) gb|EAA16201.1| ERYTHROCYTE MEMBRANE PROTEIN PFEMP3 [Plasmodium yoelii yoelii] Length = 643
- 94.7 Best-BlastP=> >nrprot 23% Identities = 354/1425 (24%), Positives = 554/1425 (38%), Gaps = 309/1425 (21%) ref|NP_772111.1| bl|5471 [Bradyrhizobium japonicum] dbj|BAC50736.1| bl|5471 [Bradyrhizobium japonicum USDA 110] Length = 4210
- 940.4 Best-BlastP=> >nrprot 60% Identities = 134/293 (45%), Positives = 176/293 (60%), Gaps = 23/293 (7%) ref|NP_931279.1| ribosomal protein L11 methyltransferase [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE16459.1| ribosomal protein L11 methyltransferase [Photobacterium luminescens subsp. laumondii TTO1] Length = 296
- 941.3 Best-BlastP=> >nrprot 85% Identities = 333/444 (75%), Positives = 381/444 (85%) ref|NP_931267.1| biotin carboxylase (A subunit of acetyl-CoA carboxylase) (ACC) [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE16447.1| biotin carboxylase (A subunit of acetyl-CoA carboxylase) (ACC) [Photobacterium luminescens subsp. laumondii TTO1] Length = 449
- 943.3 Best-BlastP=> >nrprot 72% Identities = 86/160 (53%), Positives = 117/160 (73%), Gaps = 6/160 (3%) ref|NP_760165.1| Biotin carboxyl carrier protein [Vibrio vulnificus CMCP6] gb|AAO09692.1| AE016801_11 Biotin carboxyl carrier protein [Vibrio vulnificus CMCP6] dbj|BAC95899.1| biotin carboxyl carrier protein [Vibrio vulnificus YJ016] Length = 154
- 944.3 Best-BlastP=> >nrprot 78% Identities = 93/145 (64%), Positives = 114/145 (78%) ref|ZP_00090970.1| COG0757: 3-dehydroquininate dehydratase II [Azotobacter vinelandii] Length = 147

- 946.3 Best-BlastP=> >nrprot 62% Identities = 80/201 (39%), Positives = 126/201 (62%) ref|NP_768568.1| bl1928 [Bradyrhizobium japonicum] Length
gb|AAG60905.1|AF322013_24 ID481 [Bradyrhizobium japonicum] dbj|BAC47193.1| bl1928 [Bradyrhizobium japonicum] USDA 110]
- 947.3 Best-BlastP=> >nrprot 43% Identities = 42/78 (53%), Positives = 53/78 (67%) ref|NP_768567.1| bl1927 [Bradyrhizobium japonicum] Length
gb|AAG60904.1|AF322013_23 ID479 [Bradyrhizobium japonicum] dbj|BAC47192.1| bl1927 [Bradyrhizobium japonicum] USDA 110]
- 948.3 Best-BlastP=> >nrprot 72% Identities = 88/155 (56%), Positives = 118/155 (76%) ref|ZP_00092102.1| COG1943: Transposase and inactivated
derivatives [Azotobacter vinelandii] Length = 270
- 949.3 Best-BlastP=> >nrprot 70% Identities = 322/616 (52%), Positives = 436/616 (70%), Gaps = 4/616 (0%) ref|NP_820141.1| protein-export
membrane protein SecD [Coxiella burnetii RSA 493] gb|AAO90655.1| protein-export membrane protein SecD [Coxiella burnetii RSA 493]
Length = 622
- 950.2 Best-BlastP=> >nrprot 15% Identities = 49/165 (29%), Positives = 77/165 (46%), Gaps = 13/165 (7%) emb|CAA70596.1| cinnamate 4-
hydroxylase [Phaseolus vulgaris] Length = 355
- 952.1 Best-BlastP=> >nrprot 46% Identities = 87/296 (29%), Positives = 142/296 (47%), Gaps = 12/296 (4%) gb|AAD02145.1| regulatory protein
[Pseudomonas stutzeri] Length = 300
- 953.2 Best-BlastP=> >nrprot 12% Identities = 30/118 (25%), Positives = 62/118 (52%), Gaps = 19/118 (16%) ref|NP_785847.1| esterase (putative)
[Lactobacillus plantarum WCFS1] emb|CAD64698.1| esterase (putative) [Lactobacillus plantarum WCFS1] Length = 339
- 956.2 Best-BlastP=> >nrprot 56% Identities = 102/249 (40%), Positives = 143/249 (57%), Gaps = 3/249 (1%) ref|NP_419511.1| transcriptional
regulator SkgA [Caulobacter crescentus CB15] sp|Q9R67|SKGA_CAUCR Transcriptional regulator skgA (Stationary-phase regulation of katG
protein) pir|C87335 transcription regulator SkgA [imported] - Caulobacter crescentus gb|AAF01797.1|AF170912_1 putative helix-turn-helix
transcriptional regulator SkgA [Caulobacter crescentus] gb|AAK22679.1| transcriptional regulator SkgA [Caulobacter crescentus CB15]
Length = 255
- 957.2 Best-BlastP=> >nrprot 44% Identities = 89/269 (33%), Positives = 129/269 (47%), Gaps = 3/269 (1%) ref|NP_337940.1| hydrolase, alpha/beta
hydrolase fold family [Mycobacterium tuberculosis CDC1551] gb|AAK47754.1| hydrolase, alpha/beta hydrolase fold family [Mycobacterium
tuberculosis CDC1551] Length = 310
- 959.2 Best-BlastP=> >nrprot No Hits found
- 96.6 Best-BlastP=> >nrprot 99% Identities = 276/277 (99%), Positives = 277/277 (100%) gb|AAM00632.1| unknown [Legionella pneumophila]
Length = 294
- 960.2 Best-BlastP=> >nrprot 82% Identities = 79/102 (77%), Positives = 86/102 (84%) gb|AAM00607.1| unknown [Legionella pneumophila]
Length = 121
- 964.3 Best-BlastP=> >nrprot 24% Identities = 61/202 (30%), Positives = 103/202 (50%), Gaps = 18/202 (8%) gb|AAF05325.1| unknown virulence
protein [Legionella pneumophila] Length = 205
- 965.3 Best-BlastP=> >nrprot 99% Identities = 118/118 (100%), Positives = 118/118 (100%) gb|AAQ10305.1| DotV [Legionella pneumophila]
Length = 180

- 966.2 Best-BlastP=> >nrprot 53% Identities = 95/244 (38%), Positives = 133/244 (54%), Gaps = 7/244 (2%) ref|NP_639315.1| phenol hydroxylase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM43197.1| phenol hydroxylase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 307
- 967.2 Best-BlastP=> >nrprot 71% Identities = 184/333 (55%), Positives = 242/333 (72%) ref|ZP_00032409.1| COG3588: Fructose-1,6-bisphosphate aldolase [Burkholderia fungorum] Length = 370
- 969.2 Best-BlastP=> >nrprot 67% Identities = 116/243 (47%), Positives = 168/243 (69%), Gaps = 1/243 (0%) ref|NP_819931.1| endonuclease/exonuclease/phosphatase family [Coxiella burnetii RSA 493] gb|AAO90445.1| endonuclease/exonuclease/phosphatase family [Coxiella burnetii RSA 493] Length = 255
- 97.2 Best-BlastP=> >nrprot No Hits found
- 971.2 Best-BlastP=> >nrprot No Hits found
- 972.3 Best-BlastP=> >nrprot 24% Identities = 82/304 (26%), Positives = 130/304 (42%), Gaps = 29/304 (9%) ref|NP_477218.1| loki CG10895-PB [Drosophila melanogaster] ref|NP_724241.1| loki CG10895-PC [Drosophila melanogaster] dbj|BAA28756.1| short form of nuclear kinase [Drosophila melanogaster] gb|AAL48020.1| LD27857p [Drosophila melanogaster] gb|AAN11062.1| CG10895-PB [Drosophila melanogaster] gb|AAN11063.1| CG10895-PC [Drosophila melanogaster] Length = 459
- 974.2 Best-BlastP=> >nrprot 58% Identities = 151/387 (39%), Positives = 226/387 (58%), Gaps = 8/387 (2%) ref|NP_925546.1| aspartate aminotransferase [Gloeobacter violaceus] dbj|BAC90541.1| aspartate aminotransferase [Gloeobacter violaceus] Length = 395
- 976.3 Best-BlastP=> >nrprot 58% Identities = 31/82 (37%), Positives = 51/82 (62%) ref|NP_378270.1| 341aa long conserved hypothetical protein [Sulfolobus tokodaii] Length = 341
- 977.3 Best-BlastP=> >nrprot 39% Identities = 69/181 (38%), Positives = 88/181 (48%), Gaps = 6/181 (3%) ref|NP_632394.1| chorismate mutase; prephenate dehydratase [Methanosarcina mazei Goe1] gb|AAM30066.1| chorismate mutase; prephenate dehydratase [Methanosarcina mazei Goe1] Length = 354
- 979.3 Best-BlastP=> >nrprot 40% Identities = 124/252 (49%), Positives = 162/252 (64%), Gaps = 3/252 (1%) gb|AAB97629.1| malonate decarboxylase beta subunit [Acinetobacter calcoaceticus] Length = 295
- 980.1 Best-BlastP=> >nrprot 58% Identities = 89/229 (38%), Positives = 140/229 (61%), Gaps = 3/229 (1%) ref|NP_640916.1| malonate decarboxylase gamma subunit [Xanthomonas axonopodis pv. citri str. 306] gb|AAM35452.1| malonate decarboxylase gamma subunit [Xanthomonas axonopodis pv. citri str. 306] Length = 234
- 981.2 Best-BlastP=> >nrprot 52% Identities = 60/217 (27%), Positives = 113/217 (52%), Gaps = 29/217 (13%) gb|AAF20287.1| AF121266_9 MdcE [Acinetobacter calcoaceticus] Length = 226
- 982.3 Best-BlastP=> >nrprot 64% Identities = 196/465 (42%), Positives = 301/465 (64%), Gaps = 21/465 (4%) ref|NP_819781.1| protease DO [Coxiella burnetii RSA 493] gb|AAO90295.1| protease DO [Coxiella burnetii RSA 493] Length = 451
- 983.1 Best-BlastP=> >nrprot 64% Identities = 112/239 (46%), Positives = 156/239 (65%), Gaps = 7/239 (2%) ref|NP_230359.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir||H82289 conserved hypothetical protein VC0710 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93875.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 240

- 985.2 Best-BlastP=> >nrprot 66% Identities = 148/309 (47%), Positives = 215/309 (69%), Gaps = 4/309 (1%) ref|NP_779940.1| ribosomal large subunit pseudouridine synthase D [Xylella fastidiosa Temecula1] sp|Q87AR7|RLUD_XYLFT Ribosomal large subunit pseudouridine synthase D (Pseudouridylate synthase) (Uracil hydrolyase) gb|AAO29589.1| ribosomal large subunit pseudouridine synthase D [Xylella fastidiosa Temecula1] Length = 331
- 986.3 Best-BlastP=> >nrprot 83% Identities = 55/83 (66%), Positives = 72/83 (86%), Gaps = 3/83 (3%) ref|ZP_00065010.1| COG1923: Uncharacterized host factor I protein [Microbulbifer degradans 2-40] Length = 86
- 989.3 Best-BlastP=> >nrprot No Hits found
- 99.1 Best-BlastP=> >nrprot No Hits found
- 991.2 Best-BlastP=> >nrprot 53% Identities = 104/276 (37%), Positives = 152/276 (55%), Gaps = 3/276 (1%) ref|NP_680903.1| ORF_ID:tr0112~probable hydrolase [Thermosynechococcus elongatus BP-1] db|BAC07665.1| ORF_ID:tr0112~probable hydrolase [Thermosynechococcus elongatus BP-1] Length = 285
- 992.2 Best-BlastP=> >nrprot No Hits found
- 993.2 Best-BlastP=> >nrprot 80% Identities = 285/416 (68%), Positives = 332/416 (79%), Gaps = 3/416 (0%) ref|NP_820266.1| phosphofructokinase, putative [Coxiella burnetii RSA 493] gb|AAO90780.1| phosphofructokinase, putative [Coxiella burnetii RSA 493] Length = 420
- 994.2 Best-BlastP=> >nrprot 53% Identities = 284/930 (30%), Positives = 483/930 (51%), Gaps = 57/930 (6%) ref|ZP_00126364.1| COG0784: FOG: CheY-like receiver [Pseudomonas syringae pv. syringae B728a] Length = 917
- 995.2 Best-BlastP=> >nrprot 70% Identities = 109/212 (51%), Positives = 151/212 (71%), Gaps = 6/212 (2%) ref|NP_717282.1| glutathione S-transferase family protein [Shewanella oneidensis MR-1] gb|AAN54726.1| AE015613_3 glutathione S-transferase family protein [Shewanella oneidensis MR-1] Length = 216
- 996.2 Best-BlastP=> >nrprot 79% Identities = 221/328 (67%), Positives = 266/328 (81%), Gaps = 1/328 (0%) ref|NP_717281.1| fumarylacetoacetate hydrolase family protein [Shewanella oneidensis MR-1] gb|AAN54725.1| AE015613_2 fumarylacetoacetate hydrolase family protein [Shewanella oneidensis MR-1] Length = 328
- 997.2 Best-BlastP=> >nrprot 99% Identities = 345/348 (99%), Positives = 347/348 (99%) sp|Q53407|ILLY_LEGPN 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPPD) (LEGIOLYSIN) gb|AAC32843.1| legiolysin [Legionella pneumophila] Length = 348
- 998.3 Best-BlastP=> >nrprot 69% Identities = 337/597 (56%), Positives = 425/597 (71%), Gaps = 4/597 (0%) ref|NP_819507.1| ATP-dependent DNA helicase RecQ [Coxiella burnetii RSA 493] gb|AAO90021.1| ATP-dependent DNA helicase RecQ [Coxiella burnetii RSA 493] Length = 601
- 999.2 Best-BlastP=> >nrprot 75% Identities = 225/375 (60%), Positives = 290/375 (77%) ref|ZP_00056039.1| COG1960: Acyl-CoA dehydrogenases [Magnetospirillum magnetotacticum] Length = 408

Table XIV

ORF	SEQ ID	EMBL NAME	Posit°1	Posit°2	Sens	SignalP	Name of the gene	Product of the gene	Note	Class
2402.4	4329	lpp0001	204	1562	p	-	dnaA	Chromosomal replication initiator protein DnaA		3.1
2404.2	4330	lpp0002	1576	2679	p	-	dnaN	DNA polymerase III, beta chain		3.1
2406.3	4331	lpp0003	2676	3737	p	-	recF	RecF recombinational DNA repair ATPase		3.3
1041.3	3535	lpp0004	4034	6451	p	-	gyrB	DNA gyrase, subunit B (type II topoisomerase)		3.4
1040.3	3534	lpp0005	6821	7861	m	-		unknown	Similar to peptidylarginine deiminase and related enzymes	2.2
925.3	6541	lpp0006	7864	9756	m	-	speA	unknown	similar to biosynthetic arginine decarboxylase	2.2
991.2	6583	lpp0007	9776	10621	m	-		unknown	Putative carbon-nitrogen hydrolase family protein	2.1.1
989.3	6581	lpp0008	11162	12421	m	-		unknown		6
986.3	6580	lpp0009	12609	12866	p	-		unknown	Similar to host factor-1 protein	4.4
888.3	6512	lpp0010	12894	14138	p	-		unknown	Similar to GTP-binding protein HflX	4.6
889.1	6513	lpp0011	14243	14713	m	+		unknown	Similar to thioredoxin	1.4
891.3	6514	lpp0012	14880	16457	m	-		unknown		6
5216.2	6044	lpp0013	16603	17442	p	-		unknown	Similar to other protein	5.2
3892.3	5223	lpp0014	17975	19090	p	-		unknown	Similar to conserved hypothetical protein	5.2
3895.2	5224	lpp0015	19192	20265	p	+		unknown	Similar to multidrug resistance efflux pump	1.2
5642.1	6229	lpp0016	20240	21172	p	-		unknown		6
4918.2	5900	lpp0017	21157	22062	p	-		unknown		6
4919.1	5901	lpp0018	22046	23431	p	-		unknown	similar to outer membrane efflux proteins	1.2
5644.3	6230	lpp0019	23666	25342	p	+		unknown	Similar to Legionella zinc metalloproteinase precursor	2.2
4398.2	5567	lpp0020	25563	26474	p	-		unknown	Putative integral membrane protein	5.2

Table XIV

4396.1	5566	lpp0021	26665	27144	p	-	unknown	similar to conserved hypothetical protein	5.2
4395.2	5565	lpp0022	27141	29264	p	-	unknown	Similar to conserved hypothetical protein	5.2
5380.3	6106	lpp0023	29334	29882	m	-	unknown	Putative membrane protein	5.2
341.6	4921	lpp0024	30029	30454	m	+	hbp hemin binding protein Rcp protein, confers resistance to cationic antimicrobial peptides and promotes intracellular infection		4.1
339.5	4907	lpp0025	30594	31166	m	+	rcp		
337.3	4898	lpp0026	31326	32717	p	-	unknown	similar to amino acid permease	1.2
336.1	4891	lpp0027	32727	33722	m	-	unknown	similar to low-affinity inorganic phosphate transporter	1.2
335.1	4889	lpp0028	33739	34380	m	-	unknown	similar to ubiquinone biosynthesis protein	2.5
334.5	4885	lpp0029	34603	37533	p	-	Unknown		1.3
3830.2	5191	lpp0030	37645	38535	m	-	unknown		6
3832.1	5192	lpp0031	38594	39787	m	+	unknown	Similar to aminopeptidase	2.2
3834.1	5193	lpp0032	39849	40874	m	-	unknown		6
2567.2	4437	lpp0033	41138	41899	p	-	unknown		6
2568.1	4438	lpp0034	42156	42512	p	+	unknown		6
2569.3	4439	lpp0035	42575	43297	m	-	unknown	Similar to conserved hypothetical protein	5.2
3835.2	5194	lpp0036	43511	44254	m	-	unknown	Similar to arginine transport system periplasmic binding protein	1.2
3837.4	5195	lpp0037	44415	45932	m	-	unknown	Ankyrin repeat protein	4.6
6151.1	6338	lpp0038	46159	47244	p	-	Unknown	Similar to transposase (IS4 family)	4.5
5999.1	6317	lpp0039	47270	47563	p	-	unknown	Similar to unknown proteins	5.2
4715.3	5769	lpp0040	47833	48315	p	+	unknown	Similar to hypothetical protein	5.2
4714.1	5768	lpp0041	48337	49332	m	-	unknown	Similar to conserved hypothetical protein	5.2
4713.1	5767	lpp0042	49497	49820	p	-	unknown		6
5532.2	6175	lpp0043	50133	50993	m	-	unknown	Similar to conserved hypothetical protein	5.2
5533.2	6176	lpp0044	51171	51407	m	-	unknown		6

Table XIV

1682.4	3922	lpp0045	51728	52603	p	-	unknown	Similar to sterol desaturase	2.4
1683.2	3923	lpp0046	52728	52940	m	-	unknown		6
1684.3	3924	lpp0047	53150	53548	p	-	unknown		6
4378.2	5551	lpp0048	53747	54409	p	-	unknown	Similar to antibiotic acetyltransferase	4.2
4379.1	5552	lpp0049	54406	55284	p	-	unknown	Similar to acetyltransferase	2.1.1
4381.2	5553	lpp0050	55337	56632	p	+	unknown	similar to amino acid permease family proteins	1.2
4383.2	5554	lpp0051	56714	57580	p	+	unknown	Putative integral membrane protein	5.2
2483.2	4389	lpp0052	57641	57889	m	-	unknown		6
2482.1	4388	lpp0053	58034	58516	m	-	unknown		6
2481.4	4387	lpp0054	58729	59622	m	-	unknown	Similar to probable methylisocitrate lyase	2.1.1
4600.2	5694	lpp0055	59931	60665	m	-	unknown	Similar to hypothetical protein	5.2
4601.1	5695	lpp0056	60658	61359	m	-	unknown		6
4602.3	5696	lpp0057	61465	62373	p	-	unknown	Similar to lysR family transcriptional regulator	3.5.2
5652.2	6235	lpp0058	62518	63237	p	-	unknown		6
4045.2	5320	lpp0059	63273	63833	p	-	unknown	Similar to part of sdbB protein (substrates of the Legionella pneumophila Dot/Icm system)	5.1
4043.1	5319	lpp0060	64139	64543	m	-	unknown	Similar to transcriptional regulator, MerR family	3.5.2
4042.1	5318	lpp0061	64613	65356	p	-	unknown	Similar to glutaredoxin	4.1
4041.1	5317	lpp0062	65555	66646	p	+	unknown		6
4040.1	5316	lpp0063	66766	66984	p	-	unknown		6
4039.2	5315	lpp0064	67037	68341	m	-	HipA protein, DNA binding regulator		3.5.2
4037.2	5314	lpp0065	68335	68574	m	-	hipA	Similar to transcriptional regulator HipB	3.5.2
4036.2	5313	lpp0066	68614	68898	p	-	hipB		6
4035.1	5312	lpp0067	69332	69697	p	-	unknown	Similar to plasmidic transfer origin protein TraK	4.5
4490.2	5622	lpp0068	69995	70840	m	-	unknown		6
4491.3	5623	lpp0069	71169	71336	m	-	unknown		6
4492.3	5624	lpp0070	71961	72902	p	+	unknown		6

Table XIV

4493.1	5625	lpp0071	72941	73105	p	-	Unknown	Similar to transposase (ISL3 family)	4.5
2441.2	4359	lpp0072	73331	74551	p	-	unknown	Similar to phage-related integrase proteins	4.4
2439.2	4357	lpp0073	74635	74958	p	-	unknown	Similar to phage-related proteins	4.4
2438.2	4356	lpp0074	74955	75239	p	-	unknown	Similar to transcriptional regulator	3.5.2
4496.2	5626	lpp0075	75421	76254	p	-	unknown	Similar to <i>L.pneumophila</i> LvrA protein	5.1
5605.2	6211	lpp0076	76560	76958	p	-	unknown	hypothetical gene	6
1570.4	3850	lpp0077	77084	80260	p	+	unknown	Similar to cation/multidrug efflux pump	1.2
4516.3	5639	lpp0078	80253	81398	p	+	unknown	similar to membrane-fusion protein involved in transport	1.2
1387.2	3735	lpp0079	81395	82834	p	-	unknown	Similar to outer membrane efflux protein	1.2
1388.2	3736	lpp0080	83095	83403	m	-	unknown		6
2271.1	4249	lpp0081	83452	83688	m	-	unknown	hypothetical gene	6
2270.2	4248	lpp0082	83696	83923	m	-	unknown		6
5387.1	6109	lpp0083	84154	84903	p	-	Unknown	Similar to transposase (IS5 family)	4.5
5388.1	6110	lpp0084	84891	85124	p	-	unknown		6
3953.1	5254	lpp0085	85457	86635	m	-	unknown	Similar to aspartate aminotransferase	2.2
1692.2	3929	lpp0086	86682	88673	p	-	uvrB excinuclease ABC subunit B		3.2
3950.2	5253	lpp0087	89028	90641	p	+	Unknown	regulatory protein (GGDEF and EAL domains)	1.3
5028.3	5960	lpp0088	90733	92304	m	+	unknown	similar to other proteins	5.2
5390.1	6112	lpp0089	92382	92696	m	-	unknown	Similar to conserved hypothetical protein	5.2
4021.2	5306	lpp0090	92852	93433	p	-	unknown	Similar to conserved hypothetical protein	5.2
4023.2	5307	lpp0091	93537	94847	p	-	pepP	similar to proline aminopeptidase P II	2.2
4025.1	5308	lpp0092	94837	96039	p	-	ubiH	similar to 2-octaprenyl-6-methoxyphenol hydroxylase	2.5
4026.2	5309	lpp0093	96036	97199	p	+	unknown	similar to monooxygenase	4.2

Table XIV

1451.4	3777	lpp0120	128974	130254	m	-	unknown	similar to putative xanthine/uracil permeases	1.2
1859.2	4034	lpp0121	130272	131078	m	-	unknown	Similar to conserved hypothetical protein	5.2
1858.1	4033	lpp0122	131177	131446	m	-	unknown		6
1856.3	4032	lpp0123	132053	133855	p	-	unknown		6
4574.2	5677	lpp0124	133855	134892	p	-	unknown	Similar to farnesyl-diphosphate farnesyltransferase (Squalene: synthetase)	2.4
1160.3	3610	lpp0125	135178	136374	m	-	Unknown	Similar to transposase (IS4 family)	4.5
4881.4	5879	lpp0126	136692	139913	m	-	unknown	Ankyrin repeat protein	4.6
1331.3	3705	lpp0127	140150	141358	m	-	unknown	Similar to predicted signal transduction protein. Contains EAL motifs	5.2
1332.3	3706	lpp0128	141599	143053	m	-	unknown	glycine dehydrogenase [decarboxylating] subunit 2 (glycine decarboxylase) (glycine cleavage system P-protein)	2.2
3626.1	5066	lpp0129	143047	143355	m	-	unknown	Similar to conserved hypothetical protein	5.2
3625.2	5065	lpp0130	143355	144725	m	-	unknown	glycine dehydrogenase [decarboxylating] subunit 1 (glycine decarboxylase) (glycine cleavage system P-protein)	2.2
3623.2	5064	lpp0131	144728	145105	m	-	unknown	Similar to glycine cleavage system H protein	2.2
3622.4	5063	lpp0132	145139	146221	m	-	unknown	Similar to glycine cleavage system protein T	2.2
4977.4	5932	lpp0133	146344	146823	p	-	unknown		6
4974.1	5931	lpp0134	146798	147328	m	+	unknown	Some similarity with L. pneumophila IcmL/DotI	5.1
4793.2	5824	lpp0135	147825	149564	p	-	unknown	Similar to ABC transporter, permease protein	1.2
4790.3	5823	lpp0136	149572	150870	p	-	unknown	Similar to ABC transporter, ATP- binding protein	1.2

Table XIV

4788.3	5822	lpp0137	151031	151645	m	+	dsbA	thiol:disulfide interchange protein precursor DsbA		
4980.3	5935	lpp0138	151656	152258	m	+		Unknown	similar to cytochrome c4	3.9
4979.1	5933	lpp0139	152333	152935	p	-		unknown	Similar to GTP-binding protein	1.4
2921.3	4626	lpp0140	153049	156360	p	-		unknown		4.6
327.2	4843	lpp0141	156457	158415	m	-	acsB	unknown	Highly similar to acetyl-CoA synthetase	6
328.1	4850	lpp0142	158342	159238	m	-		unknown	Similar to 3-hydroxyisobutyrate dehydrogenase	2.1.1
330.2	4862	lpp0143	159262	160761	m	-		unknown	Similar to C. burnetii methy/malonate-semialdehyde dehydrogenase MmsA	2.1.1
2919.1	4624	lpp0144	160872	161048	m	-		unknown	Weakly similar to conserved hypothetical protein	5.2
1003.3	3512	lpp0145	161226	163694	p	-		unknown	Some similarity with eukaryotic proteins, putative coiled-coil protein	6
1005.2	3513	lpp0146	163798	164529	m	-	dapB	unknown	similar to dihydrodipicolinate reductase proteins	2.2
6425.1	6380	lpp0147	164709	164894	m			Unknown	hypothetical, similar to hypothetical proteins	5.2
2917.1	4623	lpp0148	165251	165943	p	-		unknown	Similar to N-terminal part of ProQ, activator of ProP osmoprotectant transporter (truncated?)	3.5.2
2360.2	4301	lpp0149	165944	167014	p	+		unknown	Similar to hypothetical protein	5.2
2361.4	4302	lpp0150	167114	172741	m	-	sdhB	SdhB protein, substrate of the Dot/1cm system		5.1
3568.3	5025	lpp0151	172833	174257	m	-		unknown	Similar to pyruvate kinase II PykA, glucose stimulated	2.1.2
3566.1	5024	lpp0152	174241	175431	m	-	pgk	phosphoglycerate kinase		2.1.2
712.2	6419	lpp0153	175442	176434	m	-	gap	glyceraldehyde 3- phosphate dehydrogenase		
711.2	6418	lpp0154	176515	178521	m	-	tkt	unknown	Similar to transketolase	2.1.2
2335.2	4282	lpp0155	178779	180113	p	-		unknown		6
2336.2	4283	lpp0156	180177	182228	p	-	prfC	Oligopeptidase A		2.2

Table XIV

3563.3	5023	lpp0158	183008	183355	p		unknown		5.2
9.2	6521	lpp0159	183169	183672	p		unknown		5.2
7.1	6412	lpp0160	183831	187949	p	-	unknown	Similar to Wolinella succinogenes hypothetical protein	5.2
4.1	5288	lpp0161	187946	188938	p	-	unknown	Similar to Wolinella succinogenes hypothetical protein	5.2
3.1	4683	lpp0162	188945	189244	p	-	unknown	Similar to Wolinella succinogenes hypothetical protein	5.2
2.1	4112	lpp0163	189225	189818	p	-	unknown	Similar to Wolinella succinogenes hypothetical protein -RecB family exonuclease	5.2
59.1	6298	lpp0164	192785	193228	p		unknown	similar to unknown proteins	5.2
58.1	6273	lpp0165	193218	193901	m	-	prpA	Similar to putative phage repressor	3.5.2
57.1	6255	lpp0166	194054	194923	p	-	lvrA	Legionella vir region protein	5.1
55.1	6161	lpp0167	194865	195251	p	-	lvrB	Legionella vir region protein	5.1
52.1	6035	lpp0168	195264	195467	p	-	lvrC	Legionella vir region protein	3.5.2
50.1	5945	lpp0169	195464	195766	p	+	lvhB2	Legionella vir homologue protein	1.8
48.1	5827	lpp0170	195776	196057	p	-	lvhB3	Legionella vir homologue protein	1.6
47.1	5756	lpp0171	196044	198524	p	-	lvhB4	Legionella vir homologue protein	1.6
46.1	5692	lpp0172	198521	199231	p	+	lvhB5	Legionella vir homologue protein B5	4.5
9001.1	6522	lpp0173	199246	199392	p		lvhB7	Legionella vir homologue protein	1.6
45.1	5629	lpp0174	199389	199784	p	-	lvrD	Legionella vir region protein	5.1
44.1	5568	lpp0175	199788	200828	p	-	lvhB6	Legionella vir homologue protein	1.6
43.1	5494	lpp0176	200825	201541	p	-	lvhB8	Legionella vir homologue protein	1.6

Table XIV

42.1	5432	lpp0177	201538	202290	p	+	lvhB9	Legionella vir homologue protein	1.6
39.1	5227	lpp0178	202287	203378	p	-	lvhB10	Legionella vir homologue protein	1.6
37.1	5115	lpp0179	203380	204384	p	-	lvhB11	Legionella vir homologue protein	1.6
36.1	5046	lpp0180	204377	206278	p	-	lvhD4	Legionella vir homologue protein	1.6
35.1	4975	lpp0181	206376	207173	p	+	lvrE	Legionella vir region protein	5.1
34.1	4916	lpp0182	207419	208168	p	-		unknown	6
33.1	4861	lpp0183	208292	210931	m	-		unknown	4.5
30.1	4684	lpp0184	211180	211386	p	-		unknown	6
29.1	4611	lpp0185	211373	211642	p	-		unknown	4.5
27.1	4506	lpp0186	211736	212383	p	+		unknown	5.2
26.1	4457	lpp0187	212387	213196	p	-		unknown	5.2
25.1	4399	lpp0188	213223	213684	m	-		unknown	2.3
24.1	4325	lpp0189	213677	215104	m	+		unknown	5.2
20.1	4113	lpp0190	215097	215456	m	-		unknown	6
19.1	4061	lpp0191	215473	216120	m	-		unknown	3.5.2
18.1	4000	lpp0192	216289	216528	p	-		unknown	6
16.1	3869	lpp0193	216559	216765	p	-		unknown	4.4
15.1	3803	lpp0194	216714	217922	p	-		unknown	4.4
13.1	3688	lpp0195	218149	218973	p	-		unknown	5.2
11.2	3573	lpp0196	218960	219922	p	-		unknown	5.2
2622.1	4468	lpp0197	220253	222193	p	-		unknown	3.2
2605.3	4461	lpp0198	222190	224688	p	-		unknown	3.2
2620.1	4467	lpp0199	224863	225129	p	-		unknown	4.5

putative component of type IV secretion system

Highly similar to L.pneumophila TraA-like protein

some similarity with TraD protein

similar to unknown protein

similar to unknown proteins

Similar to cytosine/adenosine deaminases

similar to putative membrane proteins

Similar to transcriptional repressors (RecA-mediated autopeptidases) and prophage repressors

Similar to putative phage excisionase

Similar to phage integrase

Similar to hypothetical protein

Similar to hypothetical protein

Similar to adenine specific DNA methylase (Mod-related)

similar to Type III restriction-modification enzyme, helicase subunit

Similar to transposase

Table XIV

2619.1	4465	lpp0200	225090	225545	p		unknown	similar to transposase	4.5
2616.1	4464	lpp0201	225539	226405	p	-	unknown	Similar to unknown proteins	5.2
6117.2	6335	lpp0202	226596	229781	p	-	unknown	Ankyrin repeat protein	6
577.2	6270	lpp0203	230009	230875	p	-	Unknown	Similar to unknown proteins	5.2
3729.1	5130	lpp0204	230880	231446	m	-	unknown	Similar to conserved hypothetical proteins	5.2
3730.1	5131	lpp0205	231770	232150	m	-	unknown	Similar to C-terminal part of phage integrase	6
3731.1	5132	lpp0206	232229	232591	m	-	unknown	Similar to conserved hypothetical protein	4.4
3732.1	5133	lpp0207	233168	234034	p	-	unknown	Similar to conserved hypothetical protein	5.2
3734.1	5134	lpp0208	234326	235429	p	+	unknown	Some similarity with nucleoside hydrolase	2.3
3735.2	5135	lpp0209	235729	237378	p	-	unknown	Similar to N-terminal part of sidC	5.1
6178.1	6343	lpp0210	237675	238718	p		Unknown	Similar to transposase (ISL3 family)	4.5
4421.2	5579	lpp0211	238709	239518	p	-	unknown	similar to unknown proteins, possibly interrupted by an IS element	5.2
4422.1	5580	lpp0212	239615	239896	p	-	unknown	hypothetical gene	6
4424.1	5581	lpp0213	240007	240228	p	-	unknown		6
4425.1	5582	lpp0214	240269	240784	p	-	unknown	Similar to hypothetical protein	5.2
4427.1	5583	lpp0215	241233	241457	m	-	unknown	hypothetical protein	6
4429.2	5584	lpp0216	241674	241988	m	-	unknown		6
1827.3	4017	lpp0217	242283	243719	p	-	unknown		6
1826.2	4016	lpp0218	243980	244726	p	-	unknown		6
4920.4	5903	lpp0219	245074	245952	m	-	Unknown	regulatory protein (GGDEF domain)	1.3
1302.2	3690	lpp0220	245982	247064	m	-	Unknown	regulatory protein (EAL domain)	1.3
1303.3	3691	lpp0221	247179	247940	m	-	unknown	Similar to type I methionine aminopeptidase proteins	3.8
3570.2	5027	lpp0222	247921	248133	m	-	unknown	Similar to conserved hypothetical protein	5.2
2392.2	4323	lpp0223	248310	248789	m	+	unknown	Predicted membrane protein	6
2391.2	4322	lpp0224	249025	250002	p	-	unknown		6
3572.1	5028	lpp0225	250131	250550	m	-	unknown	Similar to conserved hypothetical protein	5.2

Table XIV

1578.3	3852	lpp0226	250975	251748	p	-	unknown	Similar to conserved hypothetical protein	5.2
1579.4	3853	lpp0227	251830	252285	m	+	unknown	Similar to conserved hypothetical protein	5.2
5044.2	5973	lpp0228	252453	253337	m	-	unknown	similar to conserved hypothetical protein	5.2
5046.2	5974	lpp0229	253604	254014	m	-	unknown	similar to unknown proteins	5.2
5047.3	5975	lpp0230	254115	254840	m	-	unknown	Similar to hypothetical protein	5.2
2739.3	4531	lpp0231	254837	255523	m	-	unknown	Similar to C-terminal part of paraquat-inducible protein	5.2
2738.2	4530	lpp0232	255591	256346	m	-	unknown	Similar to hypothetical ABC transporter (permease)	1.2
2737.2	4529	lpp0233	256612	257178	m	-	unknown	Protein with a F-box domain	6
190.3	4062	lpp0234	257395	258093	p	-	unknown		6
191.2	4068	lpp0235	258223	259083	m	-	unknown	Similar to transcriptional regulator (LysR family)	3.5.2
193.4	4079	lpp0236	259194	260243	p	-	unknown	Similar to pyoverdine biosynthesis protein PvcA	2.1.1
195.3	4092	lpp0237	260233	261069	p	-	unknown	Similar to pyoverdine biosynthesis protein PvcB	2.1.1
197.3	4100	lpp0238	261066	262508	p	-	unknown	similar to FAD monooxygenase, PheA/TfdB family	2.1.1
199.1	4108	lpp0239	262505	263653	p	+	unknown	some similarity with transporters	1.2
201.2	4116	lpp0240	263650	264882	p	-	unknown	similar to hypothetical protein	5.2
2030.2	4127	lpp0241	265040	266182	m	-	unknown		6
2041.2	4133	lpp0242	266605	267696	p	-	unknown	some similarity with methyltransferases	4.6
2039.1	4131	lpp0243	267801	268619	p	-	unknown		6
494.2	5911	lpp0244	268794	269636	m	+	unknown	Similar to protease heat shock protein	4.1
496.1	5922	lpp0245	269845	270756	p	-	unknown		6
497.1	5929	lpp0246	270803	271255	m	-	unknown		6
498.5	5934	lpp0247	271666	273144	p	-	unknown	Similar to conserved hypothetical protein	5.2
2037.3	4130	lpp0248	273404	274813	p	+	unknown	Similar to Zn metalloprotein	2.2
2733.1	4528	lpp0249	274940	275992	p	-	unknown	Similar to predicted acyl-CoA transferases	2.4
2732.1	4527	lpp0250	276189	277055	m	+	unknown		6

Table XIV

2730.1	4526	lpp0251	277434	278387	p	-	unknown	6
1188.2	3624	lpp0252	278622	280871	m	+	catalase-peroxidase	4.2
1930.3	4080	lpp0253	280991	281995	m	-	unknown	6
2049.2	4135	lpp0254	282282	283535	m	-	unknown	6
2728.1	4524	lpp0255	283927	284244	p	-	unknown	5.2
2727.2	4523	lpp0256	284496	287144	p	-	unknown	6
1213.2	3638	lpp0257	287559	288695	p	+	unknown	2.1.1
1211.3	3637	lpp0258	289073	290107	p	+	unknown	6
930.3	6545	lpp0259	290220	291590	p	-	unknown	1.4
932.1	6546	lpp0260	291590	292579	p	-	unknown	1.4
935.2	6547	lpp0261	292580	293365	m	-	unknown	5.2
936.3	6548	lpp0262	293362	293898	m	-	unknown	6
2769.2	4548	lpp0263	293888	295675	m	-	unknown	5.2
2770.1	4550	lpp0264	295758	296456	p	-	unknown	4.6
2771.2	4551	lpp0265a	296473	297642	p	-	unknown	5.2
5926.1	6307	lpp0265b	297776	298012	p	-	unknown	5.2
2772.1	4552	lpp0266	298017	298430	m	-	unknown	5.2
657.3	6389	lpp0267	298794	301679	p	-	unknown	3.8
656.3	6388	lpp0268	301698	303668	p	-	unknown	6
350.3	4976	lpp0269	303748	304335	p	-	unknown	6
351.1	4984	lpp0270	304477	304923	m	-	unknown	4.6
354.1	5005	lpp0271	304984	306399	m	-	unknown	3.2
357.2	5026	lpp0272	306494	307201	m	-	unknown	5.2
359.2	5037	lpp0273	307179	307568	m	-	unknown	5.2

similar to conserved hypothetical protein

Similar to chitin-binding protein CbpD

similar to cytochrome d ubiquinol oxidase subunit I

similar to cytochrome d ubiquinol oxidase subunit II

similar to conserved hypothetical protein

Putative membrane protein

Similar to hypothetical protein similar to oxydoreductase

similar to unknown protein (N-terminal part)

similar to unknown protein (C-terminal part)

similar to serine/threonine-protein kinase (conserved domain)

Similar to sensory protein (eukaryotic)

similar to deoxyribodipyrimidine photolyase phrB

similar to membrane protein LrgB

Predicted membrane protein, similar to conserved hypothetical protein LrgA

Table XIV

2774.1	4553	lpp0274	307674	308558	p	-	unknown	similar to transcriptional regulator, lysR family	3.5.2
2775.1	4554	lpp0275	308681	308893	p	-	unknown	Similar to conserved hypothetical protein	5.2
2777.1	4555	lpp0276	308979	310058	m	-	purK	Phosphoribosylaminoimidazole carboxylase, ATPase subunit	2.3
2778.2	4556	lpp0277	310055	310555	m	-	purE	Phosphoribosylaminoimidazole carboxylase catalytic subunit	2.3
2780.3	4558	lpp0278	310615	311454	m	-	unknown	similar to unknown protein	5.2
2781.1	4559	lpp0279	311479	311832	m	-	unknown	similar to conserved hypothetical protein	5.2
1649.4	3901	lpp0280	311846	314134	m	-	unknown	similar to unknown protein	5.2
1650.2	3902	lpp0281	314149	315669	m	-	unknown	Similar to NADH-ubiquinone oxidoreductase chain 5	1.4
2587.2	4449	lpp0282	315771	316622	p	-	unknown	similar to transcriptional regulator, lysR family	3.5.2
1940.2	4086	lpp0283	316664	318253	p	+	unknown	Similar to toxin secretion ABC transporter ATP-binding protein	1.2
1943.3	4087	lpp0284	318250	319236	p	+	unknown	Similar to RND efflux membrane fusion proteins	1.2
4561.2	5669	lpp0285	319233	320630	p	-	unknown	similar to outer membrane component of multidrug efflux pump	1.2
4560.2	5668	lpp0286	320813	321919	p	-	unknown		6
4559.1	5667	lpp0287	322090	323655	m	+	unknown	Similar to amino acid transporters	1.2
4558.1	5666	lpp0288	323803	324636	m	-	unknown		6
6072.1	6330	lpp0289	324863	324988	p	-	unknown	hypothetical gene	6
6071.1	6329	lpp0290	324918	325130	p		unknown	similar to unknown protein	5.2
4553.2	5665	lpp0291	325750	326448	p	+	unknown	Similar to 3-oxacyl-(acyl-carrier-protein) reductase	2.4
5146.2	6022	lpp0292	326541	327836	p	+	unknown	Similar to proline/betaine transporter ProP	1.2
3116.2	4752	lpp0293	327811	328203	m	-	unknown	Similar to conserved hypothetical protein	5.2
3114.2	4751	lpp0294	328441	329259	p	-	cyoA	cytochrome o ubiquinol oxidase subunit II	1.4

Table XIV

3113.1	4750	lpp0295	329262	331256	p	-	cyoB	cytochrome o ubiquinol oxidase subunit I	1.4
3110.1	4749	lpp0296	331256	331852	p	-	cyoC	Cytochrome o ubiquinol oxidase subunit III cyoC	1.4
3109.2	4748	lpp0297	331854	332192	p	-	cyoD	Cytochrome o ubiquinol oxidase subunit IV	1.4
6263.1	6357	lpp0298	332287	332469	m	-		unknown	6
3106.2	4747	lpp0299	332712	334541	m	-		Unknown	1.3
3105.2	4746	lpp0300	334546	334842	m	-		unknown	6
3104.2	4745	lpp0301	334988	337546	m	-		unknown	1.2
3102.2	4744	lpp0302	337878	338324	p	-		unknown	Similar to Fe2+/Zn2+ uptake regulation proteins
3101.1	4743	lpp0303	338633	340444	p	-		unknown	3.5.2
514.5	6021	lpp0304	340555	345045	m	-	side	SidE protein, substrate of the Dot/Icm system	6
2150.1	4193	lpp0305	345463	345945	m	-		unknown	5.1
1222.5	3642	lpp0306	346040	348019	m	-		unknown	5.2
2315.3	4271	lpp0307	348301	349095	p	-		unknown	6
2317.2	4272	lpp0308	349112	350578	p	-		unknown	2.1.1
2804.1	4569	lpp0309	350553	351905	p	-	gabT	unknown	Similar to hydrolase similar to betaine aldehyde dehydrogenase BetB similar to 4-aminobutyrate aminotransferase
2279.2	4252	lpp0310	351994	352752	p	-		unknown	4.1
1722.2	3948	lpp0311	353016	353948	p	-		unknown	2.2
1723.6	3949	lpp0312	354072	354959	p	-		unknown	6
2806.1	4570	lpp0313	355096	355695	m	-		unknown	2.2
670.1	6394	lpp0314	356025	357419	m	-		unknown	Similar to dehydrogenase similar to oxydoreductase
309.2	4736	lpp0315	357471	360830	m	-		unknown	similar to C-terminal part of conserved hypothetical protein
310.1	4742	lpp0316	361030	361755	p	-		unknown	5.2
312.3	4754	lpp0317	361996	362949	p	-		unknown	6
2807.1	4571	lpp0318	363109	363450	p	-		unknown	similar to arsenate reductase
2434.2	4354	lpp0319	363537	364691	m	-		unknown	similar to fatty acid desaturase

Table XIV

2432.2	4353	lpp0320	364810	366054	m	-	rhIE	unknown	similar to ATP-dependent RNA helicase RhIE	3.6
2808.1	4572	lpp0321	366385	366660	p	-		unknown	Similar to N-terminal part of eukaryotic RNA-binding protein precursor	4.6
2424.4	4345	lpp0322	366836	367513	p	-		unknown	Similar to unknown protein; putative membrane protein	5.2
2425.3	4346	lpp0323	367551	368189	p	-		unknown	similar to putative acetyltransferase	2.1.1
2426.2	4347	lpp0324	368323	368850	p	-		unknown		6
2810.1	4573	lpp0325	369005	370351	p	+		unknown	similar to outer membrane protein	1.1
2811.2	4574	lpp0326	370341	371378	p	-		unknown	N-terminal part similar to N- terminal part of conserved hypothetical protein	5.2
365.4	5079	lpp0327	371435	372427	p	-		unknown	similar to multidrug resistance proteins	1.2
364.2	5073	lpp0328	372604	374547	p	-		unknown		6
360.3	5047	lpp0329	374566	376350	p	-		unknown		6
2031.2	4128	lpp0330	376713	377027	p	-		Unknown	Similar to transposase (IS4 family)	4.5
3163.1	4778	lpp0331	377053	377346	p	-		unknown	similar to conserved hypothetical protein	5.2
3165.1	4779	lpp0332	377546	377944	p	-		unknown		6
3166.1	4780	lpp0333	378030	378632	m	-		unknown	Similar to C-terminal part of DNA polymerase, bacteriophage-type	3.1
3167.1	4781	lpp0334	378927	380201	p	-		unknown	Similar to transporter, MFS family	1.2
3169.1	4782	lpp0335	380322	380978	p	+		unknown	weakly similar to amidase	1.1
2488.2	4392	lpp0336	381115	382095	m	+		unknown		6
2489.2	4393	lpp0337	382142	382390	m	+		unknown		6
2490.2	4395	lpp0338	382554	383003	p	+		unknown	Similar to multicopper oxidase	4.7
4719.2	5772	lpp0339	383108	384655	m	+		unknown		6
4718.1	5771	lpp0340	384883	385317	p	-		unknown	Similar to magnesium and cobalt transport proteins	1.2
4716.2	5770	lpp0341	385332	386324	m	-		unknown	Similar to predicted hydrolase	2.1.1
2695.2	4503	lpp0342	386589	387176	p	-		unknown		

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2696.2	4504	lpp0343	387311	388810	p	-	unknown	similar to conserved hypothetical protein	5.2
1564.3	3845	lpp0344	388891	390294	p	-	pncB Nicotinate phosphoribosyltransferase		
1563.3	3844	lpp0345	390299	390919	p	-	pncA nicotinamidase/pyrazinamidase		2.5
2698.1	4505	lpp0346	391002	391385	m	-	unknown	similar to conserved hypothetical protein	2.5
2700.2	4508	lpp0347	391385	392599	m	+	unknown	Similar to transporter of the major facilitator superfamily (MFS)	5.2
2702.2	4509	lpp0348	392717	393586	p	-	unknown	Similar to transcriptional regulators	1.2
326.2	4837	lpp0349	393998	397348	p	-	sdbA SdbA protein, putative substrate of the Dot/Icm system		3.5.2
325.1	4831	lpp0350	397428	398981	p	-	Unknown	Unknown	5.1
324.3	4823	lpp0351	399047	399712	m	-	Unknown	regulatory protein (EAL domain)	6
2486.3	4391	lpp0352	399749	401272	m	-	Unknown	regulatory protein (GGDEF domain)	1.3
2704.4	4510	lpp0353	401275	402690	m	-	unknown	Similar to two-component sensor histidine kinase	1.3
2705.3	4511	lpp0354	402713	403876	m	-	unknown	Similar to conserved hypothetical protein	5.2
2706.2	4512	lpp0355	404049	404930	m	-	unknown	similar to transcriptional regulator lysR family	3.5.2
1183.4	3621	lpp0356	405129	407048	p	-	unknown	protein with ankyrin motif	6
1184.2	3622	lpp0357	407059	408243	m	+	unknown	similar to amino acid transporter	1.2
1186.2	3623	lpp0358	408311	409087	m	-	unknown	Some similarity with eukaryotic proteins	5.2
189.3	4055	lpp0359	409295	410506	p	-	unknown	Similar to NAD+-dependent formate dehydrogenase	1.4
188.1	4047	lpp0360	410611	411735	m	-	unknown		6
187.1	4041	lpp0361	411972	412655	p	-	unknown		6

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185.1	4030	lpp0362	412760	413533	p	+	unknown	similar to oxidoreductase, short chain dehydrogenase/reductase family	2.1.1
184.3	4023	lpp0363	413777	414136	p		unknown	hypothetical gene	6
1968.1	4099	lpp0364	414759	414989	p	+	unknown	signal peptide predicted	6
1966.2	4098	lpp0365	415044	415613	m	-	efp	Similar to elongation factor P	3.7.4
2709.1	4513	lpp0366	415685	416665	p	-	unknown	similar to conserved hypothetical protein	5.2
4267.5	5473	lpp0367	416734	418806	m	-	ppk	Polyphosphate kinase	2.6
1474.4	3788	lpp0368	418847	420052	m	-	unknown	Similar to conserved hypothetical protein	5.2
1473.4	3787	lpp0369	420128	420661	m	-	unknown	Weakly similar to chromate transport protein	1.2
4269.3	5474	lpp0370	420658	421278	m	-	unknown		6
1908.4	4067	lpp0371	421454	423892	p	-	unknown	similar to acyl-CoA dehydrogenase	2.4
4272.3	5476	lpp0372	424006	424698	p	-	unknown		6
4323.1	5509	lpp0373	424735	425397	m	-	unknown	similar to nucleotidyltransferase family protein	1.1
4322.1	5508	lpp0374	425394	426371	m	-	unknown	Similar to conserved hypothetical protein	5.2
4321.2	5507	lpp0375	426614	429133	p	-	unknown	Similar to organic solvent tolerance protein	4.2
4320.1	5506	lpp0376	429309	430598	p	+	surA	Similar to peptidyl-prolyl cis-trans isomerase SurA	3.8
1251.2	3659	lpp0377	430595	431569	p	-	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	2.5
1250.1	3658	lpp0378	431571	432062	p	-	folA	dihydrofolate reductase	2.5
1249.3	3656	lpp0379	432069	432614	m	-	unknown	similar to eukaryotic proteins	5.2
6247.1	6356	lpp0380	438476	439666	p	-	tufA	elongation factor Tu	3.7.4
4883.3	5880	lpp0381	439817	440188	p	-	secE	Preprotein translocase secE subunit	1.6
4884.1	5881	lpp0382	440191	440739	p	-	nusG	transcription antitermination protein NusG	3.5.4

Table XIV

4885.2	5882	lpp0383	440849	441283	p	-	rplK	50S ribosomal protein L11	3.7.1
5592.2	6205	lpp0384	441293	441988	p	-	rplA	50S ribosomal protein L1	3.7.1
2106.2	4164	lpp0385	442161	442694	p	-	rplJ	50S ribosomal subunit protein L10	3.7.1
2104.1	4163	lpp0386	442725	443105	p	-	rplL	50S ribosomal subunit protein L7/L12	3.7.1
1106.5	3577	lpp0387	443197	447303	p	-	rpoB	RNA polymerase B-subunit	3.5.3
1663.6	3912	lpp0388	447392	451597	p	-	rpoC	RNA polymerase beta subunit	3.5.3
5596.3	6207	lpp0389	451711	452091	p	-	rpsL	30S ribosomal protein S12	3.7.1
5595.2	6206	lpp0390	452112	452639	p	-	rpsG	30S ribosomal protein S7	3.7.1
4468.2	5604	lpp0391	452654	454738	p	-	fusA	translation elongation factor G	3.7.4
4466.3	5603	lpp0392	454759	455949	p	-	tufA	translation elongation factor Tu	3.7.4
4464.1	5602	lpp0393	455955	456272	p	-	rpsJ	30S ribosomal subunit protein S10	3.7.1
4463.2	5601	lpp0394	456307	456957	p	-	rplC	50S ribosomal subunit protein L3	3.7.1
4462.3	5600	lpp0395	456957	457562	p	-	rplD	50S ribosomal subunit protein L4	3.7.1
5892.1	6293	lpp0396	457559	457855	p	-	rplW	50S ribosomal subunit protein L23	3.7.1
5894.3	6294	lpp0397	457867	458694	p	-	rplB	50S ribosomal subunit protein L2	3.7.1
5895.3	6295	lpp0398	458713	458991	p	-	rpsS	30S ribosomal subunit protein S19	3.7.1
1199.4	3629	lpp0399	459001	459336	p	-	rplV	50S ribosomal subunit protein L22	3.7.1
1201.1	3630	lpp0400	459339	459995	p	-	rpsC	30S ribosomal protein S3	3.7.1
1202.2	3631	lpp0401	460012	460425	p	-	rplP	50S ribosomal protein L16	3.7.1
4133.1	5383	lpp0402	460425	460619	p	-	rpmC	50S ribosomal subunit protein L29	3.7.1

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4134.1	5384	lpp0403	460621	460875	p	-	rpsQ	30S ribosomal protein S17	3.7.1
4135.1	5385	lpp0404	460964	461329	p	-	rpIN	50S ribosomal protein L14	3.7.1
4136.1	5386	lpp0405	461342	461671	p	-	rpIX	50S ribosomal protein L24	3.7.1
4138.1	5387	lpp0406	461687	462238	p	-	rpLE	50S ribosomal protein L5	3.7.1
4139.1	5388	lpp0407	462251	462553	p	-	rpsN	30S ribosomal protein S14	3.7.1
4140.1	5389	lpp0408	462576	462971	p	-	rpsH	30S ribosomal protein S8	3.7.1
4141.1	5390	lpp0409	462989	463528	p	-	rplF	50S ribosomal subunit protein L6	3.7.1
4142.3	5391	lpp0410	463539	463898	p	-	rplR	50S ribosomal subunit protein L18	3.7.1
4143.3	5392	lpp0411	463908	464414	p	-	rpsE	30S ribosomal subunit protein S5	3.7.1
4144.3	5393	lpp0412	464417	464602	p	-	rpmD	50S ribosomal subunit protein L30	3.7.1
4145.3	5394	lpp0413	464602	465036	p	-	rpLO	50S ribosomal subunit protein L15	3.7.1
4148.3	5395	lpp0414	465033	466367	p	-	secY	preprotein translocase, SecY subunit	1.6
9003.1	6524	lpp0415	466384	466497	p	-		Similar to 50S ribosomal protein l36	3.7.1
4149.1	5396	lpp0416	466575	466931	p	-	rpsM	30S ribosomal protein S13	3.7.1
4151.1	5398	lpp0417	466955	467353	p	-	rpsK	30S ribosomal protein S11	3.7.1
4153.1	5399	lpp0418	467370	467990	p	-	rpsD	30S ribosomal subunit protein S4	3.7.1
4154.2	5400	lpp0419	468009	469001	p	-	rpoA	DNA-directed RNA polymerase alpha chain	3.5.3
5540.1	6179	lpp0420	469020	469403	p	-	rpIQ	50S ribosomal protein L17	3.7.1
5538.3	6178	lpp0421	469470	469949	m	-	ssb	Single-strand binding protein (SSB) (Helix- destabilizing protein)	

Table XIV

5453.3	6138	lpp0422	470033	471400	m	+	Unknown	putative transport protein, MFS family	1.2
3244.2	4827	lpp0423	471562	472320	p	-	Unknown	similar to 3-oxoacyl-[acyl-carrier protein] reductase	2.4
618.3	6344	lpp0424	472391	472804	p	-	Unknown	similar to acyl carrier proteins	2.4
619.1	6348	lpp0425	472804	473700	p	-	Unknown	similar to hydroxymyristoyl-(acyl carrier protein) dehydratase	2.4
621.5	6351	lpp0426	473705	474997	p	-	Unknown	similar to 3-oxoacyl-[acyl-carrier-protein] synthase II	2.4
687.5	6404	lpp0427	474998	476275	p	+	Unknown	similar to 3-oxoacyl-[acyl-carrier-protein] synthase beta chain	2.4
688.1	6405	lpp0428	476268	477113	p	-	Unknown	similar to lipid A biosynthesis acyltransferase	2.4
3243.1	4826	lpp0429	477223	477528	m	-	Unknown		6.
3242.4	4825	lpp0430	477704	480394	m	-	unknown		6
5633.3	6223	lpp0431	480705	481538	m	-	dapF	Diaminopimelate epimerase	2.2
5634.2	6224	lpp0432	481548	481676	m	+	unknown	putative lipopeptide	1.2
5636.1	6225	lpp0433	481835	482212	m	-	Unknown	Unknown	6.
5637.1	6226	lpp0434	482375	483034	p	-	Unknown	similar to phospholipase/carboxylesterase	2.4
4766.2	5805	lpp0435	483031	483465	p	-	Unknown	similar to conserved hypothetical proteins	5.2
4767.2	5806	lpp0436	483452	483724	p	-	Unknown	similar to conserved hypothetical proteins	5.2
4768.1	5807	lpp0437	483812	484126	m	+	Unknown	similar to other protein	5.2
4769.1	5808	lpp0438	484354	484764	p	-	fur	Ferric uptake regulation protein	3.5.2
4770.1	5809	lpp0439	484902	485045	p	-	unknown	similar to choline dehydrogenase (N-terminal part)	5.2
4771.2	5810	lpp0440	485188	486258	p	-	Unknown	regulatory protein (GGDEF domain)	1.3
5638.2	6227	lpp0441	486569	486955	m	+	Unknown		6.
5377.2	6104	lpp0442	487212	487811	p	-	Unknown		6.

Table XIV

3093.1	4738	lpp0464	510043	510795	m	-	trmD	unknown	Highly similar to tRNA (guanine-N1)-methyltransferase	3.6
3095.1	4739	lpp0465	510795	511304	m	-	rimM	unknown	similar to 16S rRNA processing protein RimM	3.6
3096.1	4740	lpp0466	511310	511570	m	-	rpsP	unknown	Highly similar to 30S ribosomal protein S16	3.7.1
3097.3	4741	lpp0467	511657	513033	m	-	ffh	unknown	similar to signal recognition particle protein Ffh	1.6
3960.2	5260	lpp0468	513290	513952	m	-		Unknown		6.
3959.2	5258	lpp0469	514226	515734	p	-		Unknown	Ankyrin repeat protein	6.
742.3	6431	lpp0470	516071	517474	p	+		Unknown	similar to amino acid antiporter	1.2
741.2	6430	lpp0471	517464	518054	p	-		Unknown		6.
740.2	6429	lpp0472	518258	518599	p	-		Unknown	similar to conserved hypothetical proteins	5.2
2213.2	4221	lpp0473	518813	519256	m	+		Unknown		6.
3958.1	5257	lpp0474	519275	519823	m	+	lidJ	Unknown	Predicted membrane protein, similar to hypothetical proteins similar to putative transmembrane proteins	5.1
3957.1	5256	lpp0475	520240	520443	m	+		unknown		5.2
3956.2	5255	lpp0476	520511	521239	p	+		Unknown	similar to conserved hypothetical proteins	5.2
5524.1	6170	lpp0477	521223	521768	p	-		Unknown	similar to hypothetical proteins	5.2
5523.2	6169	lpp0478	521773	522780	p	+		Unknown	similar to conserved hypothetical proteins, hypothetical cytochrome oxidase assembly protein	1.4
2400.2	4327	lpp0479	522770	523654	p	-		Unknown	similar to Polyprenyltransferase (cytochrome oxidase assembly factor)	1.4
2401.2	4328	lpp0480	523664	524305	p	+		Unknown	similar to hypothetical proteins	5.2
1476.2	3790	lpp0481	524671	525579	p	-		Unknown	similar to ribosomal protein S6 modification enzyme	3.8
1475.2	3789	lpp0482	525583	525828	m	-		Unknown	similar to hypothetical proteins	5.2
1989.2	4107	lpp0483	526144	527634	p	-	zwf	Unknown	similar to Glucose-6-phosphate 1-dehydrogenase	2.1.1
1990.1	4109	lpp0484	527603	528334	p	-	pgl	Unknown	similar to 6-phosphogluconolactonase	2.1.1
241.2	4334	lpp0485	528322	530160	p	-	edd	Unknown	similar to 6-phosphogluconate dehydratase	2.1.1

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240.1	4326	lpp0486	530135	531142	p	-	glk	Unknown	similar to glucokinase	2.1.1
239.1	4321	lpp0487	531129	531791	p	-	eda	Unknown	similar to 2-deydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	2.1.1
238.1	4315	lpp0488	531905	533326	p	-		Unknown	similar to sugar transport protein	1.2
235.2	4292	lpp0489	533416	534723	m	-		Unknown	similar to eukaryotic glucoamylase precursor (Glucan 1,4-alpha-glucosidase)	2.1.1
2969.1	4660	lpp0490	534891	535127	m	-		Unknown	similar to transcriptional regulator (XRE-family)	3.5.2
2970.2	4662	lpp0491	535214	535753	m	-		Unknown	similar to hypothetical proteins	5.2
916.3	6534	lpp0492	535881	536876	m	-	hemZ	Unknown	similar to Protoheme ferro-lyase(ferrochelataase)	2.5
917.3	6535	lpp0493	536987	537220	m	-	cspD	unknown		4.1
919.1	6536	lpp0494	537457	537870	p	-		Unknown	similar to N-terminus of Diadenosine tetraphosphate (Ap4A) hydrolase	2.3
920.2	6537	lpp0495	537973	538332	m	-		Unknown	similar to hypothetical proteins	5.2
4655.3	5728	lpp0496	538419	539771	p	+		Unknown	similar to outer membrane proteins	1.1
1353.3	3715	lpp0497	539911	540948	p	-		Unknown	similar to Multidrug resistance efflux pump	1.2
1354.2	3716	lpp0498	540926	541858	p	-		Unknown	Unknown	6.
4653.2	5727	lpp0499	541825	542724	p	-		Unknown	similar to hypothetical proteins	5.2
4652.2	5726	lpp0500	542746	543126	p	-		Unknown	putative transcriptional regulator	3.5.2
4432.2	5587	lpp0501	543128	543496	m	-		Unknown		6.
4433.1	5588	lpp0502	543821	544432	p	-		Unknown	similar to hypothetical protein	5.2
4434.1	5589	lpp0503	544586	545386	m	-		Unknown	ankyrin repeat protein	5.2
4435.4	5590	lpp0504	545657	547657	p	-		Unknown		6
451.3	5635	lpp0505	548479	549255	m	-		Unknown		6.
450.1	5630	lpp0506	549621	549833	p	-		Unknown		6.
448.1	5615	lpp0507	550004	550264	p	-	icmT	Unknown		1.6
447.2	5606	lpp0508	550265	550609	p	-	icmS	Unknown		1.6
444.2	5591	lpp0509	550709	551071	p	-	icmR	Unknown		1.6
443.3	5585	lpp0510	551162	551737	p	-	icmQ	Unknown		1.6

Table XIV

3562.3	5022	lpp0511	551924	553054	p	-	icmP/dotM	Unknown	1.6
3561.2	5021	lpp0512	553051	555402	p	-	icmQ/dotL	Unknown	1.6
874.2	6504	lpp0513	555806	556375	p	+	lphA	Unknown	1.6
873.2	6503	lpp0514	556387	556671	p	+	icmM/dotJ	Unknown	1.6
872.2	6502	lpp0515	556687	557325	p	-	icmL/dotI	Unknown	1.6
870.3	6501	lpp0516	557328	558410	p	+	icmK/dotH	Unknown	1.6
668.4	6393	lpp0517	558415	561561	p	+	icmE/dotG	Unknown	1.6
3322.2	4872	lpp0518	561576	562385	p	-	icmG/dotF	Unknown	1.6
3323.1	4873	lpp0519	562393	562977	p	-	icmC/dotE	Unknown	1.6
3324.1	4874	lpp0520	563003	563401	p	+	icmD	Unknown	1.6
434.3	5522	lpp0521	563599	564225	p	-	icmJ/dotN	Unknown	1.6
433.1	5514	lpp0522	564261	567290	p	-	icmB/dotO	Unknown	1.6
1071.3	3554	lpp0523	567388	568644	m	-	citA/tpa	proline/betaine transport protein homolog	1.2
1072.4	3555	lpp0524	568647	571568	m	-	icmF	Unknown	1.6
3326.2	4875	lpp0525	571568	572353	m	-	dotU	Unknown	1.6
5238.1	6052	lpp0526	572638	574227	m	-	purH	Unknown	2.3
940.4	6551	lpp0527	574254	575123	m	-	prmA	Ribosomal protein L11 methyltransferase	3.8
941.3	6552	lpp0528	575125	576468	m	-	accC	Biotin carboxylase (A subunit of acetyl-CoA carboxylase)	2.4
943.3	6553	lpp0529	576481	576963	m	-	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein	2.4
944.3	6554	lpp0530	576977	577414	m	-	aroQ	3-dehydroquininate dehydratase type II	2.2
3928.1	5245	lpp0531	577616	579406	p	-	dcoA	oxaloacetate decarboxylase alpha-chain	2.1.1
3929.2	5246	lpp0532	579972	581603	p	+	proA	zinc metalloproteinase precursor	2.2

similar to

phosphoribosylaminoimidazolecarboxamide formyltransferase and IMP cyclohydrolase (bifunctional)

Table XIV

3814.1	5180	lpp0533	581605	582453	m	+	Unknown	Putative lipase LipA (L.pneumophila)	2.4
969.2	6567	lpp0534	582903	583676	p	-	Unknown	similar to conserved hypothetical proteins	5.2
967.2	6566	lpp0535	583855	584865	m	-	unknown	Similar to fructose-bisphosphate aldolase	2.1.2
966.2	6565	lpp0536	585015	585749	m	-	unknown	Similar to ferredoxin--NADP reductase	1.4
965.3	6564	lpp0537	585833	586375	p	+	dotV		1.6
3815.2	5181	lpp0538	586519	586815	m	-	Unknown	conserved hypothetical protein	5.2
3816.2	5182	lpp0539	587033	587770	p	+	pssA	similar to CDP-diacylglycerol-serine O-phosphatidyltransferase (Phosphatidylserine synthase)	2.4
3818.1	5183	lpp0540	587999	588268	m	-	unknown	similar to sugar transport PTS phosphocarrier protein Hpr	1.2
3819.2	5184	lpp0541	588459	588758	m	-	Unknown	similar to putative sigma-54 modulation protein	3.5.2
4676.2	5743	lpp0542	588785	590179	m	-	rpoN		3.5.1
6029.1	6321	lpp0543	590387	590551	m	-	rpmG	RNA polymerase sigma-54 factor (sigma-L) 50S ribosomal subunit protein L33	3.7.1
4673.1	5742	lpp0544	590566	590802	m	-	rpmB	50S ribosomal protein L28	3.7.1
4672.1	5741	lpp0545	591071	591784	p	-	Unknown	similar to S-adenosylmethionine- dependent methyltransferase	3.6
4671.3	5740	lpp0546	591759	592883	p	-	Unknown	similar to endo-1,4-beta-glucanase (hypothetical)	2.1.1
5082.3	5997	lpp0547	592961	594448	p	-	Unknown	Protein with ankyrin domain	6.
1123.2	3587	lpp0548	594657	595799	p	-	hflK	protease subunit HflK	2.2
1122.1	3586	lpp0549	595802	596716	p	+	hflC	membrane protease subunit HflC	2.2
2149.4	4191	lpp0550	596851	598146	p	-	purA	Adenylosuccinate synthetase (IMP--aspartate ligase) (AdSS) (AMPSase)	2.3
5068.3	5990	lpp0551	598367	598936	p	-	Unknown	similar to hypothetical proteins	5.2

Table XIV

5069.3	5991	lpp0552	599136	599594	m	-	Unknown	similar to transcriptional regulator of arginine metabolism	3.5.2
5829.2	6284	lpp0553	599725	600459	p	+	Unknown	similar to putative glutamine-binding periplasmic protein precursor	2.2
4522.4	5644	lpp0554	600456	601103	p	-	Unknown	similar to amino acid ABC transporter permease	1.2
4521.1	5643	lpp0555	601087	601755	p	-	unknown	similar to amino acid (glutamine) ABC transporter (ATP-binding protein)	1.2
4520.1	5642	lpp0556	601752	602969	p	-	argG Argininosuccinate synthase		
1479.3	3791	lpp0557	602962	604197	p	-	argH Argininosuccinate lyase		2.2
1481.3	3793	lpp0558	604200	605315	p	-	Ornithine carbamoyltransferase		2.2
1838.2	4021	lpp0559	605404	606879	m	+	Unknown	similar to adenosine deaminase	2.3
4647.2	5722	lpp0560	607054	608169	p	+	Unknown	similar to ABC-type branched-chain amino acid transport systems, periplasmic component	1.2
4535.2	5655	lpp0561	608242	609579	m	+	unknown	similar to carboxy-terminal protease family protein	
4536.1	5656	lpp0562	609660	610802	m	+	Unknown	similar to membrane-bound metalloproteinase	2.2
4538.2	5657	lpp0563	610789	612333	m	-	gpmI	Highly similar to phosphoglycerate mutase proteins	2.1.2
4540.2	5659	lpp0564	612436	612732	m	+	Unknown		6
207.3	4148	lpp0565	612809	614080	m	+	Unknown	putative phospholipase C	
206.3	4141	lpp0566	614430	615146	p	-	Undecaprenyl pyrophosphate synthetase		1.1
205.1	4136	lpp0567	615157	615954	p	+	cdsA phosphatidate cytidyltransferase		2.4
204.1	4132	lpp0568	615987	617339	p	-	ecfE	similar to putative membrane-associated Zn-dependent protease	2.2

Table XIV

202.3	4120	lpp0569	617510	619822	p	+	Unknown	similar to protective surface antigen	5.2
732.3	6428	lpp0570	619936	620436	p	+	Unknown	similar to putative outer membrane proteins	1.1
731.2	6427	lpp0571	620450	621460	p	-	lpxD	UDP-3-O-[3-hydroxymyristoyl]glucosamine N-acetyltransferase	1.1
730.1	6426	lpp0572	621588	622040	p	-	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein]dehydratase	1.1
729.1	6425	lpp0573	622037	622807	p	-	lpxA	UDP-N-acetylglucosamine acyltransferase	1.1
728.2	6424	lpp0574	622811	623215	p	-	Unknown	Similar to integral membrane protein possibly involved in chromosome condensation	3.7.2
3024.1	4701	lpp0575	623237	624517	p	-	serS	Seryl-tRNA synthetase	6.
3023.1	4700	lpp0576	624685	624879	p	-	Unknown		6
3022.1	4699	lpp0577	625050	625313	p	-	Unknown		5.2
1268.2	3668	lpp0578	625653	626585	p	-	Unknown	Weakly similar to eukaryotic phytanoyl coA dioxygenase	6
1267.3	3667	lpp0579	626621	627433	p	-	Unknown		
1265.5	3666	lpp0580	627423	628253	m	-	Unknown	similar to oxidoreductase, aldo/keto reductase family, related to diketogulonate reductase	2.1.1
3018.1	4698	lpp0581	628692	629540	m	-	Unknown		6
3017.1	4697	lpp0582	629527	629817	m	-	Unknown		6.
3016.1	4696	lpp0583	629878	630369	m	-	Unknown		6.
3015.1	4695	lpp0584	630329	631087	m	-	Unknown	similar to methyltransferase	3.2
3014.1	4694	lpp0585	631053	631661	m	-	Unknown	Similar to adenosine phosphosulfate (APS) kinase	2.3
3013.2	4693	lpp0586	631658	632125	m	-	Unknown	similar to acetyltransferase, GNAT family	2.1.1
3011.2	4692	lpp0587	632122	633120	m	-	Unknown	weakly similar to C.burnetii hypothetical protein	5.2

Table XIV

5288.1	6069	lpp0588	633117	633527	m	-	unknown	similar to P.aeruginosa probable fosfomycin resistance protein	4.2
5289.2	6070	lpp0589	633524	634087	m	-	Unknown	similar to aminoglycoside 6 -N-acetyltransferase	4.2
5312.2	6079	lpp0590	634498	635124	p	-	IvgA	Unknown virulence protein	5.1
5313.1	6080	lpp0591	635154	635531	m	-	Unknown		6.
4897.2	5890	lpp0592	635681	636820	m	-	Unknown	similar to conserved hypothetical protein	5.2
4895.1	5889	lpp0593	637141	637515	p	+	sdhC	succinate dehydrogenase, cytochrome b556 subunit	2.1.3
4894.1	5888	lpp0594	637509	637856	p	-	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	2.1.3
1945.4	4088	lpp0595	637858	639627	p	-	sdhA	succinate dehydrogenase flavoprotein subunit	2.1.3
1946.2	4089	lpp0596	639640	640362	p	-	sdhB	succinate dehydrogenase, iron sulfur protein	2.1.3
1157.4	3607	lpp0597	640420	643230	p	-	sucA	2-oxoglutarate dehydrogenase, E1 subunit	2.1.3
3468.2	4958	lpp0598	643266	644495	p	-	sucB	dihydrolipoamide succinyltransferase, E2 subunit	2.1.3
1559.2	3841	lpp0599	644558	645721	p	-	sucC	succinyl-CoA synthetase, beta subunit	2.1.3
1557.3	3840	lpp0600	645796	646671	p	-	sucD	succinyl-CoA synthetase, alpha subunit	2.1.3
2356.2	4298	lpp0601	647094	647741	p	-	pdxH	unknown	2.5
1786.2	3991	lpp0602	648354	648725	p	-	letE	transmission trait enhancer protein LetE	4.6
1784.2	3990	lpp0603	648796	649185	m	-	Unknown	Similar to pyridoxine 5 -phosphate oxidase	6

Table XIV

1782.3	3989	lpp0604	649849	651117	p	-	Unknown	similar to putative transport proteins	1.2
5316.1	6081	lpp0605	651345	652802	p	+	Unknown	C-terminal part similar to unknown virulence protein	5.2
5123.3	6014	lpp0606	652992	653273	p	-	Unknown	similar to DNA-binding proteins Fis	3.5.2
5127.5	6015	lpp0607	653335	654282	m	-	Ribose-phosphate pyrophosphokinase		
3982.2	5277	lpp0608	654664	655263	m	+	Unknown	similar to putative outer membrane lipoproteins	2.3
3980.1	5276	lpp0609	655326	655832	p	-	Unknown	similar to phosphopantetheine adenyltransferase	1.2
3979.3	5274	lpp0610	655822	657546	p	+	unknown	similar to Gamma-glutamyltranspeptidase	2.5
3977.2	5273	lpp0611	657644	659860	m	-	Unknown	weakly similar to D-amino acid dehydrogenase, C-terminal cAMP binding motif	4.1
1494.2	3800	lpp0612	660069	660800	m	-	Unknown	similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase	2.2
1495.1	3801	lpp0613	660869	661189	m	-	unknown	similar to suppressor of groEL	2.4
1497.2	3802	lpp0614	661528	662595	m	-	unknown	Similar to DNA damage inducible protein P	3.5.2
5317.2	6082	lpp0615	663035	663655	m	-	Unknown	similar to hypothetical proteins	3.2
1606.2	3874	lpp0616	663730	664554	m	-	unknown	similar to formamidopyrimidine-DNA glycosylase MutM	5.2
1607.2	3875	lpp0617	664554	664784	m	-	Unknown	Hypothetical protein	3.2
1608.2	3876	lpp0618	664965	666152	p	-	unknown	similar to fatty acid desaturase	6.
4597.1	5690	lpp0619	666193	666591	m	-	Unknown		2.4
4598.2	5691	lpp0620	666857	667597	p	-	Unknown	similar to acetoacetyl-CoA reductase	6.
4729.3	5779	lpp0621	667776	668522	p	+	Unknown	similar to acetoacetyl-CoA reductase	2.4
4727.1	5778	lpp0622	668652	669050	p	-	Unknown	similar to hypothetical proteins	2.4
4726.1	5777	lpp0623	669257	669550	p	-	Unknown		5.2
4725.2	5776	lpp0624	669796	670866	m	+	Unknown	similar to hypothetical proteins	5.2
4724.2	5775	lpp0625	670936	671541	p	-	Unknown	similar to Bacillus subtilis spore maturation protein A	1.1

Table XIV

4721.2	5774	lpp0626	671538	672071	p	-	Unknown	similar to uncharacterized membrane protein, similar to <i>Bacillus subtilis</i> spore maturation protein B	1.1
4878.2	5877	lpp0627	672371	673804	m	-	Unknown	similar to membrane proteins related to metalloendopeptidases	2.2
2859.2	4597	lpp0628	674061	675266	p	-	tyrS	Similar to conserved hypothetical protein	3.7.2
693.1	6406	lpp0629	680614	681150	m	-	unknown		5.2
694.3	6407	lpp0630	681157	682515	m	+	gor	Glutathione reductase	4.1
2747.1	4532	lpp0631	682746	683726	m	-	add	similar to adenosine deaminase protein	2.3
2748.1	4533	lpp0632	684108	684554	p	-	unknown		6
2749.4	4534	lpp0633	684595	685848	m	+	unknown	Similar to phosphate permease	1.2
1760.4	3974	lpp0634	685858	686529	m	-	unknown	Similar to conserved hypothetical protein	5.2
1759.4	3972	lpp0635	686720	687484	p	-	unknown	Similar to hypothetical protein	5.2
3591.2	5038	lpp0636	687786	688349	p	-	unknown	Similar to conserved hypothetical protein	5.2
3592.1	5039	lpp0637	688342	688761	p	-	unknown	Similar to conserved hypothetical protein	5.2
3593.1	5040	lpp0638	688811	689704	p	-	pyrB	Similar to aspartate carbamoyltransferase	2.3
3594.1	5041	lpp0639	689818	690201	m	-	unknown		6
2421.2	4342	lpp0640	690313	691824	m	-	unknown	Similar to competence protein comM	5.2
3595.1	5042	lpp0641	691889	692149	m	-	unknown	Similar to conserved hypothetical protein	5.2
3596.1	5043	lpp0642	692294	692632	p	-	glnB	Nitrogen regulatory protein	2.2
3597.4	5044	lpp0643	692642	693223	m	-	unknown	similar to 5-formyltetrahydrofolate cyclo-ligase	2.5
6242.1	6355	lpp0644	693470	693655	p	-	unknown	similar to unknown protein	5.2
3599.5	5045	lpp0645	693669	694484	p	-	unknown	similar to aminodeoxychorismate lyase (PabC)	2.5

Table XIV

5741.1	6266	lpp0646	694511	695194	m	-	unknown	Similar to conserved hypothetical protein. Predicted membrane protein.	5.2
2657.3	4488	lpp0647	695376	697550	p	-	unknown	Similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase	2.4
2655.2	4487	lpp0648	697551	697970	p	-	unknown	similar to unknown protein	5.2
2653.2	4486	lpp0649	698057	698440	m	-	unknown		6
482.2	5846	lpp0650	698489	700231	m	-	unknown	similar to poly-beta-hydroxybutyrate synthase	2.4
481.1	5837	lpp0651	700672	701133	p	-	unknown	Similar to conserved hypothetical protein	5.2
480.3	5828	lpp0652	701126	702574	p	-	unknown	Similar to ABC transporter, permease component	1.2
1951.4	4094	lpp0653	702576	703328	p	-	unknown	Similar to ABC transporter ATP-binding protein	1.2
1950.2	4093	lpp0654	703325	704611	p	-	unknown	Similar ABC transporter, permease component	1.2
342.4	4930	lpp0655	704601	705845	p	-	unknown	similar to cysteine desulfurase and NifU protein family, possibly involved in the formation or repair of [Fe-S] clusters	2.2
343.3	4936	lpp0656	705842	706291	p	-	unknown	Similar to conserved hypothetical protein	2.5
344.1	4940	lpp0657	706363	706698	p	-	unknown	similar to putative lysyl-tRNA synthetase	5.2
346.2	4953	lpp0658	706701	707654	p	-	unknown	Similar to methyltransferase	3.6
347.1	4959	lpp0659	707727	708641	m	-	unknown	similar to a domain of alanyl-tRNA synthetase	2.1.1
349.2	4972	lpp0660	708888	709532	m	-	unknown	Similar to major facilitator family transporter	3.7.2
2652.2	4485	lpp0661	709535	710830	m	-	unknown	similar to unknown protein	1.2
2650.1	4484	lpp0662	711484	712797	p	+	unknown	similar to alcohol dehydrogenase	5.2
2521.4	4413	lpp0663	712857	713903	m	-	unknown		2.1.1
2522.1	4414	lpp0664	714104	714448	m	+	unknown		6
2523.1	4415	lpp0665	714635	715039	p	-	unknown	similar to hypothetical protein	5.2
2524.2	4416	lpp0666	715075	715764	m	-	unknown	Similar to polypeptide deformylase	2.2
2649.1	4483	lpp0667	716007	717194	p	-	unknown	Similar to Na ⁺ /H ⁺ antiporters	1.2

Table XIV

650.4	6385	lpp0668	717196	718317	p	-	unknown	similar to unknown protein	5.2
651.3	6386	lpp0669	718382	718783	m	-	unknown	similar to unknown protein	5.2
652.1	6387	lpp0670	718931	719788	p	-	unknown	similar to conserved hypothetical protein	5.2
2648.2	4482	lpp0671	720181	721272	p	+	unknown	Similar to L.pneumophila major outer membrane protein	1.1
2647.2	4481	lpp0672	721432	722004	m	-	unknown	Similar to 3-methyladenine-DNA glycosylase I	3.2
2646.1	4480	lpp0673	722321	722701	p	-	unknown		6
2645.1	4479	lpp0674	722802	723755	m	-	unknown		6
1288.2	3683	lpp0675	723866	725290	m	-	SidA protein, substrate of the Dot/Icm transport system		5.1
1915.3	4072	lpp0676	725451	727379	m	-	unknown	similar to probable transmembrane protein	5.2
1913.2	4071	lpp0677	727505	727897	m	-	unknown	Similar to hypothetical protein, predicted membrane protein	5.2
2644.1	4478	lpp0678	728034	728411	p	+	Unknown		6
2643.1	4477	lpp0679	728612	729919	p	-	unknown	Similar to unknown eukaryotic proteins	5.2
1434.3	3768	lpp0680	729945	732152	m	-	unknown	weakly similar with DNA uptake/competence proteins	1.2
2000.1	4114	lpp0681	732230	732679	m	-	type-IV pilin	competence and adherence associated protein -CAP-	1.8
290.2	4612	lpp0682	732691	736200	m	+	unknown	weakly similar to type 4 fimbrial biogenesis protein PilY1	1.8
286.2	4598	lpp0683	736213	736725	m	+	unknown	Similar to Tfp pilus assembly protein PilX	1.8
284.2	4591	lpp0684	736722	737789	m	-	unknown	Similar to Tfp pilus assembly protein PilW	1.8
283.1	4585	lpp0685	737786	738325	m	-	unknown	weakly similar with pre-pilin leader sequence	1.8
282.2	4578	lpp0686	738338	738916	m	-	unknown	similar to type-4 fimbrial pilin related protein	1.8
1882.2	4049	lpp0687	739267	740127	m	+	unknown	Similar to peptidoglycan GlcNAc deacetylase proteins	2.1.1
1883.4	4050	lpp0688	740304	741641	m	-	unknown		6
5159.2	6023	lpp0689	741941	743422	p	-	Unknown	similar to hypothetical proteins	5.2
1926.2	4077	lpp0690	743613	744242	p	-	unknown	similar to thymidine kinase	2.3

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1928.2	4078	lpp0691	744290	745561	p	-	unknown	Similar to major facilitator family transporter	1.2
813.2	6466	lpp0692	745574	746857	p	-	unknown	Similar to major facilitator family transporter	1.2
815.2	6467	lpp0693	746854	748077	p	-	deoB Phosphopentomutase Peptidase component of the HslUV protease (Heat shock protein)		2.3
3860.2	5208	lpp0694	748281	748829	p	-	hslV ATP-dependent hsl protease		4.1
3859.3	5207	lpp0695	748831	750156	p	-	hslU ATP-binding subunit HslU		4.1
2690.2	4502	lpp0696	750356	751495	p	-	unknown		6
2688.2	4500	lpp0697	751592	751930	p	-	unknown		6
1998.4	4111	lpp0698	752080	753318	m	-	unknown	similar to tRNA processing ribonuclease BN	3.6
6097.4	6333	lpp0699	753773	776812	p	-	rtxA-1 structural toxin protein RtxA		4.3
583.2	6285	lpp0700	776991	777590	p	-	wrbA unknown	Similar to flavoprotein Wrba (Trp repressor binding protein)	3.5.2
585.2	6286	lpp0701	778084	778434	p	-	unknown	Similar to conserved hypothetical protein	5.2
587.2	6287	lpp0702	778490	779272	p	-	exoA unknown	Similar to exodeoxyribonuclease	3.2
588.3	6291	lpp0703	779265	780035	p	-	xthA unknown	Similar to exodeoxyribonuclease III XthA	3.2
5600.2	6209	lpp0704	780172	780399	p	-	rpmE 50S ribosomal protein L31		3.7.1
1042.5	3536	lpp0705	780526	781761	p	-	Unknown	Similar to NADP-dependent malic enzyme	2.1.1
1044.3	3537	lpp0706	781973	783265	p	-	unknown	Similar to major facilitator family transporter	1.2
4388.1	5559	lpp0707	783246	784523	p	-	unknown	Similar to major facilitator family transporter	1.2
4387.4	5558	lpp0708	784554	785372	m	-	dam DNA adenine methylase		3.2
5598.2	6208	lpp0709	785543	786739	m	+	unknown	Similar to tyrosine-specific transport protein	1.2
5735.2	6264	lpp0710	786940	788130	m	+	unknown	Similar to tyrosine-specific transport protein	1.2
5177.2	6027	lpp0711	788141	788833	m	-	Unknown	Putative lipoprotein, similar to other proteins	1.2

Table XIV

5176.1	6026	lpp0712	789064	789264	p	-	unknown	6
915.3	6533	lpp0713	789717	790562	p	+	unknown	1.2
914.3	6532	lpp0714	790565	792307	p	-	unknown	1.2
1685.5	3925	lpp0715	792325	793446	p	-	unknown	1.2
384.5	5197	lpp0716	793632	794717	p	-	Unknown	4.5
6195.2	6350	lpp0717	794743	795036	p	-	unknown	5.2
3181.2	4792	lpp0718	795137	796207	p	-	unknown	1.2
1314.3	3695	lpp0719	796216	797655	p	+	unknown	1.2
3179.1	4790	lpp0720	797980	799761	m	+	unknown	1.1
3178.1	4789	lpp0721	799803	800456	m	-	ribulose-phosphate 3-epimerase	2.1.1
3177.1	4788	lpp0722	800670	801134	m	-	unknown	5.2
3175.1	4787	lpp0723	801131	801910	m	-	unknown	5.2
3174.1	4786	lpp0724	801903	802772	m	-	unknown	5.2
3173.1	4785	lpp0725	802778	803032	m	+	unknown	5.2
3172.3	4784	lpp0726	803369	804394	p	-	unknown	2.4
4749.2	5793	lpp0727	804510	806726	p	-	unknown	1.4
4748.1	5792	lpp0728	806768	807532	p	-	unknown	2.1.1
4746.1	5791	lpp0729	807569	807841	p	+	unknown	5.2
2442.2	4360	lpp0730	807834	809147	p	-	Unknown	2.3
2443.2	4361	lpp0731	809167	809982	m	-	unknown	5.2
2861.1	4599	lpp0732	809975	810802	m	-	unknown	5.2
1747.2	3964	lpp0733	811100	811366	p	-	unknown	6
1746.2	3963	lpp0734	811621	812373	m	-	unknown	1.2

similar to membrane protein

Similar to ABC-type multidrug transport, ATP-binding protein.

Similar to ABC transporter (permease)

Similar to transposase (IS4 family)

similar to unknown proteins

Similar to putative ABC transporter permease protein, hypothetical start codon

similar to outer membrane efflux protein

Similar to soluble lytic murein transglycosylase

Predicted membrane protein

Similar to conserved hypothetical protein

Similar to conserved hypothetical protein

Similar to hypothetical protein

Similar to predicted esterase

similar to NADH-ubiquinone oxidoreductase

similar to acetoacetate decarboxylase

Similar to unknown protein

similar to adenylate cyclase

Similar to conserved hypothetical protein

similar to conserved hypothetical protein

similar to amino acid ABC transporter, periplasmic binding protein.

Table XIV

1148.2	3602	lpp0735	812511	815252	p	-	glnE	unknown	similar to glutamine synthetase adenyltransferase	2.2
2862.1	4600	lpp0736	815538	816728	p	-		unknown	Similar to conserved hypothetical protein	5.2
2863.1	4601	lpp0737	816796	817368	p	-		unknown	similar to unknown protein	5.2
2571.2	4441	lpp0738	817361	818287	p	-		unknown	similar to ABC-type multidrug transport system, ATPase component	1.2
2570.2	4440	lpp0739	818284	819420	p	+		unknown	similar to ABC transporter, permease component	1.2
2866.1	4602	lpp0740	819490	820809	m	-		unknown	Similar to conserved hypothetical protein	5.2
2868.1	4603	lpp0741	820899	822659	m	+	dsbD/lidC	unknown	Similar to thiol:disulfide interchange protein DsbD	3.9
2869.1	4604	lpp0742	822845	823135	p	-	groES	10 kDa chaperonin (Protein Cpn10) (groES protein) (Heat shock protein A)		3.9
519.3	6032	lpp0743	823163	824809	p	-	htpB	60 kDa chaperonin (Protein Cpn60)(groEL protein)(Heat shock protein B).		3.9
520.1	6036	lpp0744	824932	825372	p	-		unknown	Weakly similar to DNA-binding ferritin-like protein (oxidative damage protectant)	5.2
521.2	6043	lpp0745	825629	827746	p	-		unknown	Similar to conserved hypothetical protein, predicted membrane protein	5.2
1438.4	3769	lpp0746	828080	829960	m	-	parE	Topoisomerase IV subunit B		3.4
2450.3	4366	lpp0747	830094	831902	p	-		unknown	Similar to ABC transporter ATP- binding protein	1.2
1819.6	4013	lpp0748	831991	836274	p	-		unknown	LigA protein(Legionella Infectivity Gene A)	6
300.2	4685	lpp0749	836632	838341	m	-	proS	Prolyl-tRNA synthetase (Proline--tRNA ligase)(ProRS)(Global RNA synthesis factor)		3.7.2
304.2	4704	lpp0750	838515	841352	p	-		unknown	Ankyrin repeat protein	4.6
1666.3	3914	lpp0751	841359	843017	m	-		unknown		6

Table XIV

3224.3	4810	lpp0752	843158	845464	m	+	unknown	Similar to inorganic transporter and to carbonic anhydrase (bi-functional)	4.7
3223.1	4809	lpp0753	845654	846505	m	-	unknown	similar to conserved hypothetical protein	5.2
3221.1	4808	lpp0754	846523	847890	m	-	tolC	similar to outer membrane protein TolC	1.2
3218.1	4807	lpp0755	847902	848552	m	-	unknown	Similar to L-isoaspartate carboxylmethyltransferase protein pcm	3.8
3217.3	4806	lpp0756	848733	849917	p	-	kbl	2-amino-3-ketobutyrate coenzyme A ligase	2.2
2600.4	4458	lpp0757	850004	851026	p	-	tdh	threonine dehydrogenase	2.2
2599.4	4456	lpp0758	851069	852742	p	-	unknown	Similar to ABC transporter, ATP-binding protein	1.2
1370.5	3725	lpp0759	852784	853395	p	-	unknown	Similar to enhanced entry protein EnhA	5.2
1369.2	3724	lpp0760	853505	853942	p	-	unknown	Similar to conserved hypothetical protein, predicted membrane protein	5.2
1367.3	3723	lpp0761	853942	854367	p	+	unknown	Similar to conserved hypothetical protein, predicted membrane protein	5.2
2122.2	4173	lpp0762	854407	855579	m	+	unknown	probable outer membrane protein	1.1
1034.3	3528	lpp0763	855636	856610	m	+	unknown	weakly similar to L. pneumophila IcmL protein	5.1
1032.3	3527	lpp0764	856623	857582	m	-	hutG	Similar to formimidoylglutamase	2.2
1030.3	3526	lpp0765	857920	858681	p	-	unknown	Similar to oxidoreductase	4.6
1028.3	3524	lpp0766	858681	859892	p	-	hutI	similar to imidazolone-5-propionate hydrolase HutI	2.2
3212.2	4805	lpp0767	859919	860614	p	+	unknown	Similar to conserved hypothetical protein	5.2
2460.4	4372	lpp0768	860614	862614	p	+	unknown	Similar to transporters	1.2
2461.2	4373	lpp0769	862645	862857	m	-	unknown	similar to putative integrase	4.5
2462.2	4374	lpp0770	862999	863223	m	-	unknown	similar to transposase, partial	4.5
2464.2	4375	lpp0771	863397	863732	p	-	Unknown	Similar to transposase (IS5 family)	4.5

Table XIV

4096.1	5355	lpp0772	863645	864127	p		Unknown	Similar to transposase (IS5 family)	4.5
4097.1	5356	lpp0773	864103	864252	m	-	unknown	similar to transposase, partial	4.5
4098.1	5357	lpp0774	864361	864633	m	-	unknown	similar to transposase, partial	4.5
4101.1	5359	lpp0775	865026	865229	m		unknown	similar to transposase	4.5
6404.1	6378	lpp0776	865196	865414	m		Unknown	Similar to transposase, partial	4.5
474.2	5787	lpp0777	865372	865704	m		unknown	similar to transposase	4.5
475.1	5794	lpp0778	865705	865884	m	-	unknown	hypothetical gene	6
4533.2	5654	lpp0779	866241	871886	p	+	unknown	Repeats in the N-terminal domain, similar to autotransporter	4.6
3285.3	4854	lpp0780	872079	873152	m	-	unknown	Similar to two-component sensor histidine kinase	1.3
3288.3	4855	lpp0781	873133	873804	m	-	unknown	Similar to two component transcriptional regulator	3.5.2
3290.1	4856	lpp0782	873953	874948	p	-	unknown		6
3291.2	4857	lpp0783	875049	875510	m	+	unknown		6
1733.3	3954	lpp0784	875599	876846	m	+	unknown	Similar to proton/sodium-glutamate symport protein	1.2
3295.2	4858	lpp0785	876968	879733	m	-	valS		3.7.2
1021.3	3520	lpp0786	879992	883039	m	-	unknown	Highly similar to multidrug efflux transporter	1.2
1440.4	3771	lpp0787	883156	884418	m	+	unknown	Similar to efflux transporter, RND family	1.2
6191.2	6349	lpp0788	884659	885063	p		unknown		6
3496.4	4974	lpp0789	885129	885566	p		unknown		6
3494.2	4973	lpp0790	885691	886002	p	+	unknown	Similar to predicted periplasmic or secreted lipoprotein	5.2
216.2	4199	lpp0791	886030	887283	p	-	glyA	Similar to serine hydroxymethyltransferase	2.2
215.1	4192	lpp0792	887286	887753	p	-	unknown	similar to unknown proteins	5.2
214.1	4184	lpp0793	887811	888254	p	-	nusB	Similar to N utilization substance protein B homolog	3.5.4
213.1	4176	lpp0794	888247	889203	p	-	thiL	Thiamine-monophosphate kinase	2.5
212.1	4170	lpp0795	889293	889775	p	-	pgpA	Phosphatidylglycerophosphate A	2.4
211.1	4166	lpp0796	889775	890827	p	-	unknown	Similar to predicted permease	1.2

Table XIV

209.2	4158	lpp0797	890819	891556	m	+	unknown	Some similarity with outer surface protein	1.8
5526.2	6171	lpp0798	891566	892204	m	+	unknown	weakly similar to outer membrane protein	1.8
2549.3	4428	lpp0799	892394	893818	p	-	unknown		6
331.2	4867	lpp0800	893870	895480	m	-	unknown	Similar to glutamine-dependent NAD(+) synthetase	2.5
333.3	4878	lpp0801	895764	899030	p	-	unknown	Similar to DNA/RNA helicases, superfamily II, SNF2 family	3.2
5690.2	6251	lpp0802	899289	899723	p	+	unknown	Similar to conserved hypothetical protein	5.2
4972.4	5930	lpp0803	899901	901283	p	-	dnaB	Replicative DNA helicase	3.1
4968.4	5928	lpp0804	901285	902358	p	-	unknown	similar to alanine racemase 1	2.2
6188.2	6347	lpp0805	902431	902880	p	+	unknown	similar to surface antigens (17 kDa)	5.2
5521.2	6168	lpp0806	903188	903622	p	-	unknown	Similar to conserved hypothetical protein	5.2
3684.3	5107	lpp0807	903731	904918	p	+	unknown	similar to unknown proteins	5.2
3685.1	5108	lpp0808	905030	905326	p	-	unknown	similar to unknown proteins	5.2
3686.1	5109	lpp0809	905323	906873	p	-	Unknown	regulatory protein (GGDEF domain)	1.3
3687.1	5110	lpp0810	907025	908014	p	-	lipA	Lipoic acid synthetase LipA	2.5
3688.1	5111	lpp0811	908326	908607	m	-	unknown	similar to conserved hypothetical protein	5.2
776.3	6452	lpp0812	909490	910998	m	-	iraB	di/tripeptide transporter homolog IraB	1.2
778.2	6453	lpp0813	911037	911855	m	-	iraA	small-molecule methyltransferase IraA	4.6
779.4	6454	lpp0814	912015	913397	p	-	unknown	Similar to LPS biosynthesis protein	5.1
4119.2	5372	lpp0815	913397	914158	p	-	hisF	Similar to imidazole glycerol phosphate synthase subunit HisF	2.2
4118.3	5371	lpp0816	914155	914796	p	-	hisH	similar to Imidazole glycerol phosphate synthase subunit HisH	2.2
4116.3	5370	lpp0817	914809	915507	p	-	neuA	CMP-N-acetylneuraminic acid synthetase	1.1

Table XIV

4115.1	5369	lpp0818	915504	916526	p	-	neuB	N-acetylneuraminic acid condensing enzyme	1.1
1764.3	3975	lpp0819	916526	917659	p	-	neuC	N-acetylglucosamine 2- epimerase	1.1
1765.4	3976	lpp0820	917649	918257	p	-		unknown	2.1.1
1818.4	4012	lpp0821	918268	919770	p	-		unknown	1.1
								Similar to acetyl transferase similar to polysaccharide biosynthesis protein	
4113.1	5368	lpp0822	919860	920423	p	-	rmIC	dTDP-4-dehydrorhamnose 3,5-epimerase	2.1.1
4112.1	5367	lpp0823	920424	921308	p	-	rmID	dTDP-4-keto-L-rhamnose reductase	2.1.1
4111.2	5366	lpp0824	921268	922347	p	-	rmIB	dTDP-D-glucose 4,6- dehydratase	2.1.1
5500.1	6162	lpp0825	922386	923885	p	-	gpi	Glucose-6-phosphate isomerase	2.1.2
5499.1	6160	lpp0826	924040	924915	p	-	rmIA	glucose-1-phosphate thymidyltransferase	2.1.1
5498.1	6159	lpp0827	924936	925892	p	-		unknown	2.1.1
								similar to NAD dependent epimerase/dehydratase family protein	
5497.1	6158	lpp0828	925876	926880	p	+	wecA	alpha-N- acetylglucosaminyltransfer ase	2.1.1
6110.1	6334	lpp0829a	926995	927237	p	+		unknown	1.1
								Similar to N-terminal part of Legionella hypothetical protein	5.1
5496.2	6157	lpp0829b	927224	927763	p	-		unknown	5.1
								Similar to central part of Legionella hypothetical protein	
4965.2	5926	lpp0829c	927739	928236	p	-		unknown	5.1
								Similar to C-terminal part of Legionella hypothetical protein	
4966.2	5927	lpp0830	928337	930133	m	-		unknown	5.1
1935.4	4083	lpp0831	930136	931254	m	-		unknown	5.1
1934.4	4082	lpp0832	931265	932266	m	-		unknown	5.1
4782.3	5819	lpp0833	932256	933347	m	-		unknown	1.1
								Similar to sialic acid synthase	
5528.2	6172	lpp0834	933360	934079	m	-		unknown	5.1
5060.2	5984	lpp0835	934395	935912	p	-		unknown	5.1
5061.4	5985	lpp0836	936145	937827	p	-		unknown	5.1
								ABC transporter of LPS O- antigen, Wzm	
4156.3	5401	lpp0837	937793	938644	p	-	wzm		1.2

Table XIV

4157.2	5402	lpp0838	938641	940065	p	-	wzt	ABC transporter of LPS O- antigen, Wzt unknown	Similar to putative glycosyltransferase	1.2
4158.1	5403	lpp0839	940071	941219	p	+		unknown		5.1
4159.1	5404	lpp0840	941233	942123	m	-		unknown		1.1
1359.2	3719	lpp0841	942904	943977	p	-	lag-1	O-acetyltransferase	similar to glycosyltransferase	1.1
4160.4	5405	lpp0842	944090	944983	m	-		unknown	similar to glycosyl transferase	1.1
4161.4	5406	lpp0843	944977	945996	m	-		unknown	similar to glyoxalase II	4.1
5530.2	6174	lpp0844	946208	946915	p	-		unknown		3.5.2
5256.2	6060	lpp0845	947474	947668	p	-	csrA	global regulator CsrA	Similar to O-antigen acetylase	1.1
3827.2	5190	lpp0846	947794	949776	m	-		unknown		
3826.1	5189	lpp0847	949939	950934	m	-	birA	biotin-[acetylCoA carboxylase] holoenzyme synthetase and biotin operon repressor		
2457.2	4369	lpp0848	950938	951675	m	-		unknown	Similar to phosphopantetheinyl transferase	3.5.2
2456.2	4368	lpp0849	951757	952710	p	-	accA	acetyl-CoA carboxylase carboxyl transferase subunit alpha		2.4
3824.2	5188	lpp0850	952703	953998	p	-		unknown		2.4
3822.2	5187	lpp0851	954348	954884	p	-		unknown	Similar to cell cycle protein MesJ	1.7
3821.1	5186	lpp0852	955223	956389	p	-		unknown		6
2320.3	4274	lpp0853	956386	957828	p	-		unknown	Similar to alginate o- acetyltransferase AlgI	1.1
2319.3	4273	lpp0854	957927	959303	m	-	sdhL	unknown	Similar to L-serine dehydratase	2.2
2409.3	4333	lpp0855	959508	960209	p	+	mip	macrophage infectivity potentiator		3.9
2410.2	4335	lpp0856	960375	961634	p	+		unknown	Similar to AmpG protein	1.2
2795.1	4566	lpp0857	961746	962012	p	-		unknown	Similar to transposase	4.5
540.3	6115	lpp0858a	962033	962356	p	-		unknown	similar to transposase, partial	4.5
539.3	6111	lpp0858b	962379	962978	p	-		unknown	similar to transposase, partial	4.5
538.1	6105	lpp0859	963489	964139	p	-		unknown		6
537.3	6101	lpp0860	964419	964805	p	+		unknown	similar to unknown proteins	5.2
262.4	4466	lpp0861	964909	966252	m	-	nadA	unknown	similar to quinolinate synthetase A	2.5
263.1	4472	lpp0862	966327	967976	m	-	nadB	L-aspartate oxidase		2.5

Table XIV

264.2	4476	lpp0863	967973	969343	m	-	purB	adenylosuccinate lyase		2.3
829.2	6474	lpp0864	969496	971199	p	+		unknown	Similar to sulfate transporter	1.2
2794.2	4565	lpp0865	971402	973105	m	-		unknown	Similar to acyl-CoA dehydrogenase	2.4
2793.1	4564	lpp0866	973335	974333	m	+		unknown	Similar to hydrolase	4.6
2791.1	4563	lpp0867	974558	976945	p	-	ppsA	unknown	similar to phosphoenolpyruvate synthase	2.1.2
2788.1	4562	lpp0868	977187	978626	p	+		unknown	Similar to Na(+)/H(+) antiporter	1.2
2785.1	4561	lpp0869	978623	979465	p	-	nadC	nicotinate-nucleotide pyrophosphorylase		2.5
1865.3	4040	lpp0870	979462	980553	p	-		UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase		
1864.3	4039	lpp0871	980528	981943	p	-		unknown	Similar to succinyl-diaminopimelate desuccinylase	1.1
2784.3	4560	lpp0872	982035	982352	p	+		unknown	Similar to other proteins	2.2
4841.2	5855	lpp0873	982548	983585	p	-	mreB	Rod shape-determining protein MreB		5.2
4837.1	5854	lpp0874	983563	984471	p	-	mreC	Rod shape-determining protein MreC		1.1
4836.1	5853	lpp0875	984468	984947	p	-	mreD	Rod shape-determining protein MreD		1.1
4835.4	5852	lpp0876	984883	985485	m	-		unknown	Similar to ribosomal large subunit pseudouridine synthase (Pseudouridylylase synthase)	
5650.3	6234	lpp0877	985746	986444	p	-		unknown		3.6
5649.1	6233	lpp0878	986554	987810	p	-	icd	isocitrate dehydrogenase		6
5647.1	6232	lpp0879	988212	988547	p	-		unknown	Similar to ATP-dependent Clp protease adaptor protein ClpS	2.1.3
5645.2	6231	lpp0880	988579	990846	p	-	clpA	ATP-dependent Clp protease ATP-binding subunit ClpA		4.1
6002.2	6318	lpp0881	991147	992232	p	-		Unknown	Similar to transposase (IS4 family)	4.5

Table XIV

6186.1	6346	lpp0882	992258	992551	p	-	unknown	Similar to unknown proteins	5.2
4618.1	5704	lpp0883	992707	993486	p	-	unknown	Similar to lipopolysaccharide biosynthesis glycosyltransferase	1.1
4616.3	5703	lpp0884	993489	994739	p	+	unknown	Similar to putative O-antigen biosynthesis protein	1.1
4615.3	5702	lpp0885	994740	995075	m	+	unknown	hypothetical gene	6
5479.2	6149	lpp0886	995245	995844	m	-	unknown	Similar to uncharacterized membrane protein	5.2
3747.2	5143	lpp0887	995841	996743	m	+	unknown	similar to peptidase proteins	2.2
3748.1	5144	lpp0888	996752	998083	m	-	xseA Exonuclease VII, large subunit		2.3
3750.2	5145	lpp0889	998233	999957	p	+	unknown	similar to outer membrane protein	1.1
3752.2	5146	lpp0890	999908	1000642	p	+	unknown	similar to unknown proteins	5.2
3753.2	5147	lpp0891	1000658	1002577	p	+	Unknown	regulatory protein (GGDEF and EAL domains)	1.3
3754.2	5148	lpp0892	1002713	1003438	p	+	unknown		6
3756.2	5149	lpp0893	1003416	1004756	p	-	unknown	Similar to flavin-containing monooxygenases	2.1.1
4469.2	5605	lpp0894	1004849	1005697	m	-	unknown	similar to oxidoreductases, short-chain dehydrogenase/reductase family	2.1.1
795.2	6459	lpp0895	1006173	1006949	m	-	trpC indole-3-glycerol phosphate synthases		2.2
4470.1	5607	lpp0896	1006942	1007976	m	-	trpD anthranilate phosphoribosyltransferase		2.2
1457.2	3781	lpp0897	1007954	1008532	m	-	trpG Anthranilate synthase component II		2.2
1456.2	3780	lpp0898	1008566	1009291	m	-	unknown	Similar to ABC transporter, ATP-binding protein	1.2
1455.2	3779	lpp0899	1009288	1009797	m	+	unknown	Similar to conserved hypothetical protein	5.2
4471.3	5608	lpp0900	1009778	1010347	m	+	unknown	Similar to conserved hypothetical protein	5.2
5978.2	6312	lpp0901	1010344	1010871	m	-	unknown	Similar to conserved hypothetical protein	5.2

Table XIV

5903.2	6301	lpp0902	1010885	1011847	m	-	kdsD	unknown	Similar to arabinose 5-phosphate isomerase	1.1
5696.2	6254	lpp0903	1012215	1013012	p	-		unknown	Similar to ABC transporter, ATP-binding protein	1.2
5695.1	6253	lpp0904	1013005	1013787	p	-		unknown	Similar to permease of ABC transporter	1.2
5694.2	6252	lpp0905	1013788	1014264	p	+		unknown	similar to unknown protein	5.2
5489.2	6154	lpp0906	1014272	1014880	p	+		unknown	similar to unknown protein	5.2
4341.3	5524	lpp0907	1014883	1015164	p	-		unknown	weakly similar to anti-anti-sigma factor	3.5.1
4342.1	5525	lpp0908	1015554	1015799	p	-		unknown	Similar to conserved hypothetical protein	5.2
4344.1	5526	lpp0909	1015792	1017060	p	-	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase		
4345.1	5527	lpp0910	1017057	1017815	p	-		unknown	Similar to conserved hypothetical protein	1.1
1484.2	3795	lpp0911	1018004	1018681	m	-		unknown	Highly similar to ABC transporter, ATP-binding protein	5.2
1485.4	3796	lpp0912	1018678	1019928	m	+		unknown	Similar to conserved hypothetical protein	1.2
4848.3	5859	lpp0913	1019928	1020944	m	+		unknown	similar to membrane-fusion protein	5.2
4847.2	5858	lpp0914	1021334	1021927	p	+		unknown		1.2
1096.3	3570	lpp0915	1022123	1023538	p	-	fleQ	transcriptional regulator FleQ		6
1094.1	3569	lpp0916	1023582	1023863	m	-		unknown		3.5.2
1093.3	3568	lpp0917	1024086	1025024	m	-		unknown		6
4564.2	5670	lpp0918	1025169	1025771	p	-	ccmA	heme exporter protein CcmA	Similar to protease	2.2
2597.4	4454	lpp0919	1025768	1026448	p	-	ccmB	heme exporter protein CcmB		1.2
3159.2	4775	lpp0920	1026662	1027417	p	+	ccmC	heme exporter protein CcmC		1.2
3158.1	4774	lpp0921	1027338	1027559	p	-	ccmD	heme exporter protein CcmD		1.2
3157.1	4773	lpp0922	1027565	1027996	p	+	ccmE	cytochrome c-type biogenesis protein CcmE		1.4

Table XIV

3153.3	4772	lpp0923	1027993	1029945	p	+	ccmF	cytochrome C-type biogenesis protein CcmF	1.4	
3152.1	4771	lpp0924	1029942	1030475	p	+	ccmG	cytochrome C biogenesis protein	1.4	
2085.2	4157	lpp0925	1030475	1030876	p	+	ccmH	Cytochrome c-type biogenesis protein CcmH	1.4	
2083.2	4156	lpp0926	1030869	1031555	p	+		Unknown	similar to cytochrome c-type biogenesis protein	1.4
2082.2	4155	lpp0927	1031545	1031748	p	-		unknown	Similar to conserved hypothetical protein	5.2
1853.2	4031	lpp0928	1031804	1032208	p	+		unknown	Similar to outer membrane lipoprotein	1.1
9002.1	6523	lpp0929	1032403	1032954	m			unknown	Similar to methyladenine DNA glycosylase	3.2
998.3	6589	lpp0930	1032964	1034790	m	-		unknown	similar to ATP-dependent DNA helicase RecQ	3.3
999.2	6590	lpp0931	1034904	1036058	p	-		unknown	similar to acyl-CoA dehydrogenase	2.4
1000.2	3509	lpp0932	1036075	1036851	p	-		Unknown	similar to enoyl-CoA hydratase/carnithine racemase	2.4
1542.2	3831	lpp0933	1036854	1037912	p	-		unknown	similar to enoyl-CoA hydratase/isomerase family protein	2.4
1539.2	3829	lpp0934	1038078	1038944	m	+		unknown		6
1230.2	3648	lpp0935	1039168	1040748	p	-	prfC	peptide chain release factor 3		3.7.5
1231.3	3649	lpp0936	1040814	1041197	m	-		unknown		6
4773.3	5811	lpp0937	1041332	1042729	m	+	pntB	NAD(P) transhydrogenase subunit beta (Pyridine nucleotide transhydrogenase subunit beta)		1.4
4774.1	5812	lpp0938	1042753	1043049	m	-	pnaB	NAD(P) transhydrogenase subunit beta (Pyridine nucleotide transhydrogenase subunit alpha II)		1.4

Table XIV

4775.2	5813	lpp0939	1043042	1044175	m	-	pntA	pyridine nucleotide transhydrogenase, alpha subunit		2.3
4776.3	5814	lpp0940	1044569	1045123	m	-		unknown	Similar to uncharacterized proteins	5.2
6093.1	6332	lpp0941	1045377	1045652	m	-		unknown		6
2060.3	4142	lpp0942	1045949	1047082	p	-		Unknown	regulatory protein (GGDEF domain)	1.3
2062.2	4143	lpp0943	1047144	1047785	m	+		unknown		6
2065.2	4144	lpp0944	1048268	1048702	p	-		unknown	predicted transmembrane protein	6
2066.5	4145	lpp0945	1048826	1049272	p	-		unknown		6
2067.5	4146	lpp0946	1049399	1050475	p	-		unknown	similar to glycosyl hydrolase	1.1
4068.2	5336	lpp0947	1050990	1052270	p	-		unknown	Similar to amino acid transporter	1.2
4303.1	5497	lpp0948	1052594	1053727	m	-	dapE	Succinyl-diaminopimelate desuccinylase		2.2
4302.1	5496	lpp0949	1053720	1054550	m	-	dapD	2,3,4,5-tetrahydropyridine- 2,6-dicarboxylate N- succinyltransferase		2.2
4301.1	5495	lpp0950	1054554	1055447	m	-		unknown	Similar to acetyltransferase	2.2
1420.2	3761	lpp0951	1055514	1056665	m	-	metB	unknown	Similar to cystathionine beta-lyase	4.6
1421.3	3762	lpp0952	1056814	1059129	p	-		Unknown	Similar to cystathionine beta-lyase regulatory protein (GGDEF and EAL domains)	2.2
5446.3	6135	lpp0953	1059431	1060780	p	-		unknown	Similar to kynurenine 3- monooxygenase	1.3
5447.1	6136	lpp0954	1060998	1061750	p	-		unknown	Similar to unknown proteins	2.2
1834.4	4020	lpp0955	1061707	1063077	p	-		unknown	Similar to eukaryotic cytokinin oxidase	5.2
5448.1	6137	lpp0956	1063427	1063936	p	-		unknown		4.6
4571.2	5674	lpp0957	1063942	1064319	p	-		unknown		6
2576.2	4442	lpp0958	1064401	1065360	m	+		unknown	Similar to putative sodium/calcium antiporter	6
2578.2	4443	lpp0959	1065633	1066337	m	-		unknown		1.2
4572.2	5675	lpp0960	1066576	1067643	m	-	mutY	unknown	Similar to A/G-specific adenine glycosylase	5.1
						-				3.2

Table XIV

4573.4	5676	lpp0961	1067640	1069181	m	+	unknown	Similar to conserved hypothetical protein	5.2
5904.2	6302	lpp0962	1069595	1070251	p	-	unknown		6
5010.2	5952	lpp0963	1070262	1071158	p	+	unknown		6
5015.2	5953	lpp0964	1071374	1071712	p	-	unknown	Similar to hypothetical protein	5.2
5460.1	6142	lpp0965	1071687	1072778	p	+	unknown	Similar to protease	2.2
3974.2	5272	lpp0966	1072898	1073443	p	-	unknown	Similar to hypothetical protein	5.2
3972.2	5271	lpp0967	1073653	1074396	p	-	unknown	Similar to 3-hydroxyacyl-CoA dehydrogenase type II	2.4
3971.2	5270	lpp0968	1074453	1074950	m	-	unknown	Similar to unknown protein	5.2
3970.1	5269	lpp0969	1074967	1075287	m	-	flgM	Similar to negative regulator of flagellin synthesis (Anti-sigma-28 factor)	3.5.2
3969.1	5267	lpp0970	1075378	1076079	m	+	flgA	flagellar basal body P-ring biosynthesis protein FlgA	1.5
3968.1	5266	lpp0971	1076166	1076573	p	-	unknown	similar to cytochrome c-type protein	1.4
3967.1	5265	lpp0972	1076650	1077207	p	+	unknown	Similar to enhanced entry protein EnhA	5.1
3966.1	5264	lpp0973	1077494	1078264	p	-	unknown	Similar to putative transcriptional regulator, homolog of Bvg accessory factor	3.5.2
3965.1	5263	lpp0974	1078882	1079340	p	-	unknown	similar to conserved hypothetical protein	5.2
3964.1	5262	lpp0975	1079352	1080278	p	-	unknown	Similar to S-adenosyl-methyltransferase MraW	2.1.1
3962.2	5261	lpp0976	1080275	1080613	p	-	unknown	similar to cell division protein FtsL	1.7
5462.3	6143	lpp0977	1080994	1082655	p	-	ftsI	Peptidoglycan synthetase FtsI precursor	1.1
643.3	6381	lpp0978	1082676	1084127	p	-	murE	Similar to UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase	1.1
644.2	6382	lpp0979	1084172	1085224	m	-	pdxB	similar to erythronate-4-phosphate dehydrogenase	2.5
645.4	6383	lpp0980	1085221	1085880	m	-	unknown		5.2

Table XIV

647.5	6384	lpp0981	1086129	1086776	p	-	unknown	similar to unknown protein	5.2
4859.2	5864	lpp0982	1086816	1088060	p	-	unknown		6
4860.1	5865	lpp0983	1088145	1088216	p	-	unknown	hypothetical gene	6
5515.3	6166	lpp0984	1088469	1089218	p	-	Electron transfer flavoprotein beta-subunit (Beta-ETF)		1.4
3942.2	5252	lpp0985	1089232	1090170	p	-	Electron transfer flavoprotein, alpha subunit		
623.2	6354	lpp0986	1090182	1091303	p	-	unknown	Similar to alanine dehydrogenase	2.2
622.3	6353	lpp0987	1091375	1093759	m	+	unknown	Similar to peptidoglycan synthetase; penicillin-binding protein 1A	1.1
5514.2	6165	lpp0988	1093909	1094916	m	-	unknown		6
5398.3	6114	lpp0989	1095333	1096397	p	-	Tfp pilus assembly protein, ATPase PilM		1.8
3555.2	5017	lpp0990	1096401	1096949	p	-	Tfp pilus assembly protein PilN		1.8
3554.4	5016	lpp0991	1096963	1097562	p	-	Tfp pilus assembly protein PilO		1.8
1895.6	4059	lpp0992	1097559	1098143	p	+	Tfp pilus assembly protein PilP		1.8
1896.5	4060	lpp0993	1098147	1100243	p	+	type IV pilus (Tfp) assembly protein PilQ		1.8
3551.1	5015	lpp0994	1100689	1101216	p	+	shikimate kinase I		2.2
3550.1	5014	lpp0995	1101203	1102312	p	-	3-dehydroquinate synthase		2.2
3548.2	5013	lpp0996	1102309	1103760	p	-	unknown	similar to unknown protein	5.2
3547.1	5012	lpp0997	1103869	1104300	p	-	unknown	Similar to universal stress protein A	4.1
3545.1	5011	lpp0998	1104424	1105410	p	-	Riboflavin biosynthesis protein RibF (Riboflavin kinase/FMN adenylyltransferase)		2.5
1490.4	3798	lpp0999	1105523	1108318	p	-	Isoleucyl-tRNA synthetase		3.7.2
2233.3	4231	lpp1000	1108315	1108779	p	+	Lipoprotein signal peptidase		1.6

Table XIV

2232.1	4230	lpp1001	1109078	1109641	m	-			unknown	Similar to keto-hydroxyglutarate aldolase	2.1.1
1280.3	3677	lpp1002	1109818	1112007	m	-	lidA		LidA protein, substrate of the Dot/1cm system		5.1
1366.3	3722	lpp1003	1112249	1115374	m	-			unknown		6
3629.2	5067	lpp1004	1115589	1116524	p	-			unknown	Similar to GTPases	4.6
3193.2	4797	lpp1005	1116514	1117203	p	-	recO		DNA repair protein recO		3.2
3191.1	4796	lpp1006	1117259	1118434	m	-			unknown		6
3190.1	4795	lpp1007	1118596	1119483	m	-			unknown	similar to other proteins	5.2
2159.2	4198	lpp1008	1119775	1120521	p	-	pdxJ		Pyridoxal phosphate biosynthetic protein pdxJ		
1615.2	3878	lpp1009	1120508	1122325	p	-			unknown	Similar to 2-oxoglutarate ferredoxin oxidoreductase alpha subunit	2.5
2160.2	4200	lpp1010	1122309	1123277	p	-			unknown	Similar to 2-oxoglutarate ferredoxin oxidoreductase beta subunit	2.1.1
418.4	5421	lpp1011	1123665	1124339	m	+			unknown	Predicted membrane protein, similar to transporter	1.2
419.2	5426	lpp1012	1124558	1125364	p	-			unknown	Similar to hydrolase	2.1.1
421.2	5438	lpp1013	1125376	1126818	p	-	tldD		TldD protein		2.1.1
422.3	5442	lpp1014	1126864	1127742	p	-			unknown	Similar to conserved hypothetical protein	5.2
1841.2	4025	lpp1015	1127769	1129436	p	-			unknown	Similar to long-chain-fatty-acid--CoA ligase	2.4
3186.2	4794	lpp1016	1129415	1132876	m	-	mfd		Transcription-repair coupling factor		3.5.3
3184.3	4793	lpp1017	1132953	1134215	m	-			unknown	Similar to conserved hypothetical protein	5.2
1048.3	3539	lpp1018	1134219	1135397	m	+			unknown		6
1047.2	3538	lpp1019	1135394	1136293	m	+			unknown	Similar to hypothetical protein	5.2
2330.2	4280	lpp1020	1136515	1138536	p	-	lig		DNA ligase		3.1
2333.3	4281	lpp1021	1138665	1140821	p	-			unknown	Similar to extracellular solute-binding protein	4.6
5030.2	5962	lpp1022	1140818	1141795	p	-			unknown	Similar to ABC transporter, permease protein	1.2
3927.2	5244	lpp1023	1141819	1143165	p	-			unknown	Similar to ABC transporter, permease protein	1.2

Table XIV

3404.2	4919	lpp1049	1172850	1173656	m	-	unknown	6	
3406.2	4920	lpp1050	1174294	1174938	p	+	unknown	6	
5322.2	6087	lpp1051	1174951	1175262	m	-	unknown	5.2	similar to unknown proteins
5321.2	6086	lpp1052	1175314	1175574	m	-	unknown	5.2	similar to unknown protein
4914.3	5897	lpp1053	1175704	1175988	p	+	unknown	6	
4913.2	5896	lpp1054	1176324	1177259	m	-	unknown	6	
677.6	6397	lpp1055	1177462	1179441	m	+	unknown	5.2	Similar to conserved hypothetical protein
675.6	6396	lpp1056	1179438	1179767	m	+	unknown	6	
673.3	6395	lpp1057	1179961	1181514	m	-	unknown	5.2	Putative membrane protein similar to conserved hypothetical protein
3575.2	5030	lpp1058	1181517	1182884	m	+	unknown	5.2	Similar to conserved hypothetical protein; signal peptide predicted
3574.1	5029	lpp1059	1182894	1183868	m	-	unknown	5.2	Similar to conserved hypothetical protein
1089.2	3563	lpp1060	1183861	1186611	m	-	unknown	5.2	similar to unknown proteins
1090.1	3565	lpp1061	1186621	1186968	m	+	unknown	5.2	similar to unknown proteins
1091.2	3566	lpp1062	1186925	1188184	m	+	unknown	5.2	Similar to conserved hypothetical protein
1092.3	3567	lpp1063	1188181	1188957	m	-	unknown	5.2	Similar to conserved hypothetical protein
5031.2	5963	lpp1064	1188944	1189600	m	-	unknown	5.2	Similar to conserved hypothetical protein
5032.1	5964	lpp1065	1189593	1189955	m	-	Unknown	6	
5033.1	5965	lpp1066	1189967	1190332	m	+	unknown	6	
5034.2	5966	lpp1067	1190329	1190595	m	-	unknown	6	
5319.1	6084	lpp1068	1190595	1190921	m	-	unknown	6	
5318.2	6083	lpp1069	1190931	1191563	m	-	unknown	5.2	C-terminal part similar to C-terminal part of conserved hypothetical protein
4132.3	5382	lpp1070	1191554	1191985	m	-	unknown	5.2	Similar to conserved hypothetical protein
4131.4	5381	lpp1071	1191985	1192806	m	+	unknown	5.2	similar to unknown protein
4130.3	5380	lpp1072	1192799	1193383	m	+	unknown	6	
4129.1	5378	lpp1073	1193380	1193793	m	+	unknown	1.8	similar to PilL protein

Table XIV

4128.1	5377	lpp1074	1193786	1194004	m	-	unknown	similar to carbon storage regulator	3.5.2
4127.1	5376	lpp1075	1193998	1194510	m	-	unknown	Similar to Legionella LvrB protein	5.1
4126.2	5375	lpp1076	1194362	1195264	m	-	unknown	Similar to LvrA protein	5.1
4123.2	5374	lpp1077	1195431	1195685	p	-	unknown	Similar to phage repressor	4.4
682.3	6401	lpp1078	1195761	1196723	p	-	unknown	similar to DNA modification methylase	3.2
681.4	6400	lpp1079	1196727	1197470	m	-	unknown		6
680.3	6399	lpp1080	1197572	1198027	m	-	unknown	Similar to very-short-patch-repair endonuclease vsr	3.2
678.3	6398	lpp1081	1198125	1199183	m	-	unknown		6
4955.4	5919	lpp1082	1199195	1200490	m	-	unknown	Similar to major facilitator family transporter	1.2
4954.2	5918	lpp1083	1200495	1201013	m	-	unknown	Similar to peptide deformylase	3.8
4952.1	5917	lpp1084	1200994	1201569	m	-	unknown		6
4951.2	5916	lpp1085	1201598	1202089	m	-	unknown		6
5382.1	6107	lpp1086	1202296	1202541	p	-	unknown		6
4764.2	5804	lpp1087	1202564	1202782	p	-	unknown	Similar to putative transcriptional regulator	3.5.2
4763.2	5803	lpp1088	1203051	1204295	m	-	unknown	Similar to prophage integrase	4.4
1847.3	4029	lpp1089	1204670	1206475	p	-	unknown		6
3588.2	5036	lpp1090	1206588	1207193	p	-	unknown	Similar to methyltransferase	2.1.1
3586.2	5035	lpp1091	1207525	1208634	p	-	unknown	similar to conserved hypothetical protein	5.2
1229.3	3646	lpp1092	1208718	1209173	p	-	unknown		6
1227.1	3645	lpp1093	1209729	1210397	p	-	unknown	Similar to beta-phosphoglucosylase	2.1.1
2383.4	4318	lpp1094	1210551	1210757	p	+	unknown		6
1390.5	3738	lpp1095	1210905	1211363	p	-	unknown		6
1391.1	3739	lpp1096	1211486	1212088	p	-	unknown	Similar to other protein	5.2
1392.2	3740	lpp1097	1212164	1212487	m	-	Unknown	Similar to transposase (IS5 family)	4.5
3584.1	5034	lpp1098	1212577	1212771	m	-	Unknown	Similar to transposase (IS5 family)	4.5
131.2	3694	lpp1099	1213052	1213525	m	-	unknown		6
139.6	3737	lpp1100	1214119	1218525	p	-	Unknown	Ankyrin repeat protein	6.
2609.2	4463	lpp1101	1219613	1220581	p	-	unknown		6

Table XIV

2607.2	4462	lpp1102	1220717	1221931	p	+	unknown	Putative secreted protein	6
3489.2	4971	lpp1103	1221940	1222932	m	-	unknown		6
1582.2	3856	lpp1104	1223130	1223633	p	-	unknown	similar to Peptide methionine sulfoxide reductase msrB	3.8
1581.4	3855	lpp1105	1223732	1224994	m	-	unknown		6
1156.3	3606	lpp1106	1225330	1226628	m	-	unknown	Putative membrane protein	5.2
1153.1	3605	lpp1107	1226823	1227242	m	-	unknown	Putative membrane protein	5.2
1152.2	3604	lpp1108	1227429	1228310	m	-	unknown		6
3488.1	4970	lpp1109	1228551	1230611	m	-	unknown	Some similarity with eukaryotic protein	6
3486.1	4969	lpp1110	1230904	1231038	m	-	unknown	hypothetical protein	6
3485.1	4968	lpp1111	1231171	1231866	p	-	unknown		6
3484.1	4967	lpp1112	1231960	1232598	m	-	unknown		6
3483.3	4966	lpp1113	1232814	1233419	m	-	unknown	Similar to hypothetical proteins regulatory protein (GGDEF and EAL domains)	5.2
1809.4	4008	lpp1114	1233896	1236223	m	-	Unknown		1.3
3481.2	4965	lpp1115	1236289	1236561	m	-	unknown	similar to other proteins	5.2
3480.4	4964	lpp1116	1236566	1238218	m	-	unknown	similar to other protein, ATP binding site	5.2
833.3	6477	lpp1117	1238638	1240986	p	+	unknown	similar to chitinase	2.1.1
2116.2	4168	lpp1118	1241095	1241568	m	-	unknown	Similar to B. subtilis PaIA	
499.2	5938	lpp1119	1241660	1242775	m	+	unknown	transcriptional repressor of sporulation	3.5.2
500.2	5946	lpp1120	1243043	1244107	p	+	Major acid phosphatase Map (histidine-acid phosphatase)	similar to D-alanyl-D-alanine carboxypeptidase	1.1
501.2	5951	lpp1121	1244305	1245039	p	-	unknown	PIID-dependent secreted protein, tartrate-sensitive acid phosphatase	2.6
502.3	5956	lpp1122	1245241	1245621	m	-	unknown		6
503.3	5961	lpp1123	1245903	1247231	p	+	unknown	similar to membrane-bound lytic murein transglycosylase	1.1
3161.1	4777	lpp1124	1247357	1248118	m	-	unknown	Similar to amino acid ABC transporter (amino acid binding protein)	1.2
3160.1	4776	lpp1125	1248354	1248944	m	-	unknown		6
1049.2	3540	lpp1126	1249226	1249921	p	-	unknown	Similar to amino acid ABC transporter	1.2

Table XIV

1050.4	3541	lpp1127	1250105	1253536	p	-	unknown	Some similarity with eukaryotic proteins	5.2
2368.5	4307	lpp1128	1253631	1255088	m	-	unknown	Similar to long-chain acyl-CoA synthetase	2.4
1778.5	3984	lpp1129	1255222	1255686	p	-	unknown	Similar to guanine deaminase	2.3
1775.3	3983	lpp1130	1256114	1257673	p	-	unknown		6
3801.2	5172	lpp1131	1257838	1259289	m	+	ladC	adenylate cyclase	2.3
3800.4	5171	lpp1132	1259451	1259777	m	-	unknown		6
							cyclopropane fatty acyl phospholipid synthase (Cyclopropane fatty acid synthase) (CFA synthase)		
791.5	6458	lpp1133	1259942	1261069	m	-	cfa		
3798.1	5170	lpp1134	1261123	1261503	m	-	unknown		2.4
3797.1	5169	lpp1135	1261720	1262772	m	-	unknown	Similar to 2-nitropropane dioxygenase	6
3796.3	5168	lpp1136	1262750	1263361	m	-	unknown	Similar to transcriptional regulator, (TetR family?)	4.2
3793.3	5167	lpp1137	1263531	1264433	p	+	unknown	Similar to hypothetical protein	3.5.2
3792.1	5166	lpp1138	1264540	1264761	m	+	unknown		5.2
3791.1	5165	lpp1139	1264987	1265940	m	-	unknown		6
								Similar to spermidine/putrescine-binding periplasmic protein precursor potD (SPBP)	6
3789.2	5164	lpp1140	1266221	1267243	m	-	potD		1.2
3788.1	5163	lpp1141	1267240	1268007	m	-	potC	Similar to spermidine/putrescine transport system permease protein potC. Putative integral membrane protein	
3785.2	5162	lpp1142	1268004	1268852	m	-	potB	Similar to spermidine/putrescine transport system permease protein PotB	1.2
3784.2	5161	lpp1143	1268818	1269912	m	-	potA	Similar to spermidine/putrescine transport system ATP-binding protein PotA	1.2

Table XIV

3783.1	5160	lpp1144	1270081	1270374	m	-	unknown	Hypothetical protein, similar to endonuclease	3.2
2355.2	4297	lpp1145	1270574	1271458	m	-	unknown	Similar to dehydrogenase	2.1.1
3780.2	5159	lpp1146	1271801	1272271	m	-	unknown		6
1505.4	3807	lpp1147	1272563	1274872	p	-	unknown		6
1507.3	3808	lpp1148	1275002	1276483	p	-	unknown	Similar to thermostable carboxypeptidase 1	2.2
3454.1	4950	lpp1149	1276607	1277047	p	-	unknown	Similar to acetyltransferase	2.1.1
3453.1	4949	lpp1150	1277368	1278852	p	-	unknown	Putative coiled-coil protein	6
3451.1	4948	lpp1151	1279030	1279812	p	-	unknown	similar to E. coli Ada protein (O6- methylguanine-DNA methyltransferase)	6
3450.2	4947	lpp1152	1279909	1280979	p	-	unknown		3.2
5135.2	6020	lpp1153	1281056	1282528	m	-	unknown		6
2545.2	4426	lpp1154	1282739	1283563	m	-	unknown		6
2546.4	4427	lpp1155	1283589	1285076	m	+	unknown	Similar to amine oxidase	2.2
3933.3	5248	lpp1156	1285562	1286644	p	-	unknown		6
1261.2	3664	lpp1157	1286884	1288563	p	-	unknown	Similar to eukaryotic pyruvate decarboxylase	2.1.1
1264.3	3665	lpp1158	1288621	1289817	m	+	unknown	Similar to aminopeptidase	2.2
4485.2	5618	lpp1159	1290224	1290988	p	+	unknown	Similar to L.pneumophila putative lipase LipB	2.4
4484.1	5617	lpp1160	1291137	1291871	p	-	unknown	Some similarity with eukaryotic proteins	6
895.3	6517	lpp1161	1292240	1293277	p	-	unknown	similar to putative drug metabolite transport protein (DMT family)	1.2
894.3	6516	lpp1162	1293379	1293624	m	-	unknown		6
2220.2	4224	lpp1163	1293956	1294606	p	-	unknown	Similar to predicted phosphoribosyl transferase	2.3
4319.2	5505	lpp1164	1294673	1295404	m	+	unknown	similar to other proteins	5.2
1126.3	3590	lpp1165	1295575	1296861	p	-	unknown	Similar to permeases of the major facilitator superfamily (MFS)	1.2
1125.2	3589	lpp1166	1296873	1298027	p	-	unknown	Similar to acetylornithine deacetylase	2.2
1124.2	3588	lpp1167	1298353	1299069	p	-	unknown	Weakly similar to uridine kinase	2.3
4316.4	5504	lpp1168	1299134	1301122	m	-	unknown	Some similarity with eukaryotic proteins	5.2

Table XIV

4508.4	5634	lpp1169	1301406	1301891	p	-	unknown	Similar to conserved hypothetical protein regulatory protein (GGDEF and EAL domains)	5.2
1105.2	3576	lpp1170	1302012	1304318	m	-	Unknown		1.3
4211.2	5439	lpp1171	1304470	1305813	m	-	unknown	Similar to unknown protein	5.2
4212.1	5440	lpp1172	1305885	1306961	p	-	unknown	similar to Pyruvate formate-lyase activating enzyme	2.1.1
1137.2	3597	lpp1173	1307020	1307439	p	-	unknown		6
1136.3	3596	lpp1174	1307601	1309073	p	+	unknown	Similar to conserved hypothetical protein, similar to C-terminal part of EnhC protein	5.2
4214.3	5441	lpp1175	1309172	1310758	p	-	unknown	Similar to Pseudomonas sensor protein PilS (member of the 2 component response regulator PilS/PilR involved in the regulation of the expression of the type 4 fimbriae)	1.3
544.2	6133	lpp1176	1310755	1312083	p	-	unknown	Similar to type 4 fimbriae expression regulatory protein PilR (two-component response regulator)	3.5.2
543.1	6131	lpp1177	1312513	1312758	p	-	unknown		6
2468.2	4377	lpp1178	1313196	1314131	m	-	unknown	similar to putative hydrolase	2.1.1
2469.2	4378	lpp1179	1314410	1315846	m	+	unknown	similar to putative protease	2.2
2471.3	4380	lpp1180	1315909	1316982	p	-	Riboflavin biosynthesis protein RibD		2.5
1832.4	4019	lpp1181	1316967	1317581	p	-	Riboflavin synthase alpha chain		2.5
1831.3	4018	lpp1182	1317578	1318786	p	-	Riboflavin biosynthesis protein RibA		2.5
3721.1	5129	lpp1183	1318794	1319261	p	-	riboflavin synthase beta chain (6,7-dimethyl-8-ribityllumazine synthase)		2.5
3465.2	4956	lpp1184	1319387	1321024	p	+	CTP synthase		2.3

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3463.1	4955	lpp1185	1321021	1321845	p	-	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase (Phospho-2-dehydro-3-deoxyoctonate aldolase) (3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase) (KDO-8-phosphate synthetase) (KDO 8-P synthase)	2.4
3461.4	4954	lpp1186	1322050	1323909	p	-		unknown	6
2293.5	4259	lpp1187	1324001	1326388	p	-		unknown	6
1409.3	3751	lpp1188	1326772	1327545	p	+		unknown	Similar to competence lipoprotein comL precursor
1410.2	3753	lpp1189	1327693	1328631	m	-		unknown	Similar to recombinase associated protein RdgC
3459.4	4952	lpp1190	1328749	1330623	m	+		unknown	Similar to low affinity potassium transport system protein Kup
3455.3	4951	lpp1191	1330651	1331634	m	-		unknown	6
1602.2	3872	lpp1192	1331712	1332884	p	-		unknown	5.2
1601.3	3871	lpp1193	1333009	1334157	p	+		unknown	Similar to unknown protein
5282.4	6068	lpp1194	1334297	1335022	p	-		unknown	Similar to N-acetyl-beta-glucosaminidase
3771.2	5156	lpp1195	1335111	1335734	m	-	hisI	phosphoribosyl-AMP cyclohydrolase (PRA-CH) / phosphoribosyl-ATP pyrophosphatase (PRA-PH)	2.1.1
854.4	6490	lpp1196	1335731	1336498	m	-	hisF	Imidazole glycerol phosphate synthase subunit HisF (IGP synthase cyclase subunit)	5.2
853.1	6489	lpp1197	1336492	1337211	m	-	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	2.2

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852.3	6488	lpp1198	1337205	1337804	m	-	hisH	Imidazole glycerol phosphate synthase subunit HisH (IGP synthase glutamine amidotransferase subunit)	2.2
3772.2	5157	lpp1199	1337801	1338859	m	-	hisB	histidinol- phosphatase/misazoglyc erol-phosphate dehydratase	2.2
1101.4	3574	lpp1200	1338837	1339931	m	-	hisC	Histidinol-phosphate aminotransferase (Imidazole acetol- phosphate transaminase)	similar to histidinol-phosphate aminotransferase
1102.2	3575	lpp1201	1339932	1341227	m	-	hisD	histidinol dehydrogenase	2.2
2255.2	4241	lpp1202	1341233	1342114	m	-	hisG	ATP phosphoribosyltransferase	2.2
3778.2	5158	lpp1203	1342111	1342407	m	-		unknown	Weakly similar to E. coli Trp operon repressor
5550.3	6185	lpp1204	1342784	1344316	p	-	cydA	cytochrome d ubiquinol oxidase subunit I	1.4
5552.2	6186	lpp1205	1344332	1345468	p	-	cydB	cytochrome d ubiquinol oxidase subunit II	1.4
4409.1	5576	lpp1206	1345694	1346326	m	-	pyrE	orotate phosphoribosyltransferase	2.3
4407.1	5575	lpp1207	1346575	1346808	p	-		unknown	Similar to cold shock proteins
4406.1	5574	lpp1208	1347319	1347891	p	-		unknown	similar to unknown protein
4405.1	5573	lpp1209	1348051	1348506	p	-		unknown	Similar to conserved hypothetical protein
4404.1	5572	lpp1210	1348536	1348955	m	-		unknown	Similar to transcriptional regulator, MarR family
4403.2	5571	lpp1211	1349033	1349821	p	-		unknown	Similar to conserved hypothetical protein
4402.2	5570	lpp1212	1349818	1350366	p	-		unknown	Similar to acetyltransferase
2598.3	4455	lpp1213	1350490	1351149	m	+		unknown	similar to putative amino acid (threonine) efflux protein

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5115.2	6012	lpp1214	1351439	1352398	p	-	unknown	Similar to transcriptional regulator, MarR family	3.5.2
5116.3	6013	lpp1215	1352456	1353019	p	-	unknown	Similar to conserved hypothetical protein	5.2
5554.3	6187	lpp1216	1353408	1353659	p	+	unknown	hypothetical gene	6
5555.3	6188	lpp1217	1353674	1354309	p	-	unknown		6
6052.1	6326	lpp1218	1354320	1354946	m	-	unknown	similar to unknown protein	5.2
5201.2	6038	lpp1219	1354960	1355628	m	-	unknown	Similar to thiocyanate hydrolase gamma subunit	4.2
5202.2	6039	lpp1220	1355628	1355936	m	-	unknown	Similar to thiocyanate hydrolase alpha subunit	4.2
5204.2	6040	lpp1221	1355937	1356362	m	-	unknown	Similar to thiocyanate hydrolase beta subunit	4.2
4444.2	5595	lpp1222	1356712	1358019	p	-	unknown	similar to unknown protein	5.2
4442.1	5594	lpp1223	1358164	1359099	m	-	hemF oxygen-dependent coproporphyrinogen III oxidase		2.5
4441.1	5593	lpp1224	1359315	1359707	p	-	flgB Flagellar basal-body rod protein FlgB		1.5
4440.1	5592	lpp1225	1359710	1360132	p	-	flgC Flagellar basal-body rod protein FlgC		1.5
1863.2	4038	lpp1226	1360143	1360820	p	-	flgD Flagellar basal-body rod modification protein FlgD		1.5
1862.2	4037	lpp1227	1360934	1362247	p	-	flgE Flagellar hook protein FlgE		1.5
801.3	6460	lpp1228	1362258	1363004	p	-	flgF flagellar biosynthesis protein FlgF		1.5
802.3	6461	lpp1229	1363155	1363940	p	-	flgG flagellar biosynthesis protein FlgG		1.5
803.3	6462	lpp1230	1363953	1364645	p	+	flgH flagellar L-ring protein precursor FlgH		1.5
5206.1	6041	lpp1231	1364684	1365787	p	+	flgI flagellar P-ring protein precursor FlgI		1.5
3142.2	4764	lpp1232	1365799	1366674	p	-	flgJ flagellar biosynthesis protein FlgJ		1.5
1532.3	3826	lpp1233	1366724	1368673	p	-	flgK flagellar hook-associated protein 1		1.5
1533.1	3827	lpp1234	1368677	1369912	p	-	flgL flagellar hook-associated protein FlgL		1.5

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1246.2	3655	lpp1235	1370107	1371846	p	-	unknown	Similar to conserved hypothetical protein	6	
1244.2	3654	lpp1236	1372499	1373563	p	+	unknown		6	
1417.1	3758	lpp1237	1373611	1374066	p	-	unknown		5.2	
1418.3	3759	lpp1238	1374169	1375941	m	+	unknown		1.2	
2954.4	4646	lpp1239	1376030	1377661	m	-	unknown	Similar to electron transfer flavoprotein-ubiquinone oxidoreductase	1.4	
601.5	6319	lpp1240	1377897	1379708	p	-	unknown		Similar to multidrug resistance ABC transporter ATP-binding protein	1.2
598.2	6313	lpp1241	1379791	1380108	p	+	unknown	Similar to conserved hypothetical protein	5.2	
597.2	6311	lpp1242	1380144	1380515	p	+	unknown		6	
596.3	6310	lpp1243	1380572	1382287	m	-	sfca		malate oxidoreductase	2.1.1
2955.2	4647	lpp1244	1382367	1382750	p	-	unknown		5.1	
2958.2	4648	lpp1245	1382753	1383511	p	-	surE	Acid phosphatase SurE (Stationary phase survival protein)	2.6	
2959.1	4649	lpp1246	1383530	1384273	p	+	nlpD	novel lipoprotein homolog NlpD		1.1
2960.1	4651	lpp1247	1384359	1385384	p	-	rpoS	RNA polymerase sigma factor RpoS	3.5.1	
2961.1	4652	lpp1248	1385487	1386737	m	-	hmgA	Homogentisate 1,2-dioxygenase	2.2	
2962.1	4653	lpp1249	1386884	1387627	p	-	unknown	Similar to conserved hypothetical protein	5.2	
2495.2	4398	lpp1250	1387627	1388151	p	-	ruvC		Crossover junction endodeoxyribonuclease	3.3
2493.2	4397	lpp1251	1388148	1388747	p	-	ruvA		holliday junction DNA helicase	
2492.2	4396	lpp1252	1388797	1389117	p	+	unknown		similar to sensor histidine kinase	6
938.3	6550	lpp1253	1389158	1390762	m	-	unknown	6		
937.3	6549	lpp1254	1391044	1392459	m	+	unknown	similar to two component response regulator		1.3
1589.3	3861	lpp1255	1392456	1393133	m	-	unknown		3.5.2	

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1590.1	3863	lpp1256	1393194	1393739	m	+	unknown	similar to intracellular septation protein	1.7
1591.4	3864	lpp1257	1393982	1395421	m	+	unknown	Similar to membrane bound lytic murein transglycosylase	1.1
2963.2	4654	lpp1258	1395535	1396299	m	-	gloB hydroxyacylglutathione hydrolase (glyoxalase II)		2.5
2964.1	4655	lpp1259	1396303	1397151	m	-	unknown	Similar to conserved hypothetical protein	5.2
2965.1	4656	lpp1260	1397437	1397646	p	-	unknown		6
2966.1	4657	lpp1261	1397649	1398503	m	-	Fold methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase		2.5
2967.1	4658	lpp1262	1398590	1398790	m	-	unknown		6
2968.3	4659	lpp1263	1399059	1401752	p	-	fimV FimV protein		1.8
5455.1	6139	lpp1264	1401804	1402271	m	-	unknown	Similar to conserved hypothetical protein	5.2
2156.3	4197	lpp1265	1402271	1403569	m	-	unknown	Similar to conserved hypothetical protein	5.2
1740.3	3960	lpp1266	1403813	1404601	p	-	truA tRNA-pseudouridine synthase I		3.6
1739.2	3958	lpp1267	1404602	1405225	p	-	trpF N-(5-phosphoribosyl)anthranilate isomerase		2.2
1738.3	3957	lpp1268	1405227	1406426	p	-	trpB tryptophan synthase beta subunit		2.2
1547.2	3833	lpp1269	1406452	1407270	p	-	trpA tryptophan synthase, alpha subunit		2.2
1545.3	3832	lpp1270	1407267	1408922	p	-	glnS glutamine tRNA synthetase		3.7.2
3311.1	4868	lpp1271	1408932	1410302	p	-	cysS cysteine tRNA synthetase		3.7.2
2235.2	4232	lpp1272	1410481	1412394	p	-	unknown	Similar to hypothetical sulfatase	4.7
3312.1	4869	lpp1273	1412524	1412838	p	-	unknown		6
5534.3	6177	lpp1274	1412939	1414423	m	-	lspE type II protein secretion ATPase LspE		1.6

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126.2	3662	lpp1294	1440177	1441604	m	-	flaA	flagelline	1.5
465.2	5724	lpp1295	1442014	1442898	p	-	accD	Similar to acetyl-CoA carboxylase beta subunit	2.4
464.2	5716	lpp1296	1442879	1444165	p	-	folC	Similar to dihydrofolate:folypolyglutamate synthetase FolC	2.5
462.2	5705	lpp1297	1444162	1444950	p	+		Similar to conserved hypothetical protein	5.2
460.2	5693	lpp1298	1444931	1445464	p	-		Similar to colicin V production protein Dede	4.3
459.3	5687	lpp1299	1445439	1446074	m	-	nadD	Similar to nicotinate-nucleotide adenylyltransferase NadD	2.5
458.3	5680	lpp1300	1446062	1447087	m	-		Similar to DNA polymerase III, delta subunit HolA	3.1
2943.1	4640	lpp1301	1447089	1447580	m	+		Similar to rare lipoprotein B RlpB	1.2
2942.1	4639	lpp1302	1447681	1450152	m	-	leuS	leucyl-tRNA synthetase	3.7.2
2941.1	4638	lpp1303	1450218	1451753	m	-		Similar to apolipoprotein N- acyltransferase (ALP N- acyltransferase) (copper homeostasis protein CutE)	3.8
1215.3	3639	lpp1304	1451907	1452995	p	-		Similar to dehydrogenase	4.6
1220.3	3641	lpp1305	1453005	1454525	p	-		Similar to aldehyde dehydrogenase	2.1.1
2103.2	4162	lpp1306	1454645	1457014	p	+		Similar to 3-hydroxyacyl-CoA dehydrogenase	2.4
1638.2	3893	lpp1307	1457030	1458214	p	-	fadA	Similar to 3-ketoacyl-CoA thiolase (thiolase I, acetyl-CoA transferase)	2.4
1639.4	3894	lpp1308	1458327	1459502	m	-		unknown	6
1635.4	3891	lpp1309	1459664	1462561	m	-	sidG	SidG protein, substrate of the Dot/Icm system	4.6
5481.1	6151	lpp1310	1462790	1463920	p	+		unknown	5.2
4665.2	5736	lpp1311	1464059	1466437	m	-		Unknown	1.3
4288.2	5485	lpp1312	1466752	1467720	m	+	lspK	type II secretory pathway protein	1.6
4289.2	5486	lpp1313	1467707	1468324	m	+	lspJ	type II secretory pathway protein LspJ	1.6
								similar to unknown protein regulatory protein (GGDEF and EAL domains)	1.3

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4291.1	5488	lpp1314	1468321	1468698	m	+	lspI	type II secretory pathway protein LspI	1.6	
770.3	6447	lpp1315	1468695	1469180	m	-	lspH	type II secretory pathway protein LspH	1.6	
771.4	6448	lpp1316	1469167	1469589	m	-	lspG	type II secretory pathway protein LspG	1.6	
772.4	6449	lpp1317	1469693	1470892	m	-	lspF	type II secretory pathway protein LspF	1.6	
774.3	6450	lpp1318	1470989	1472398	p	-	glnA	glutamine synthetase	2.2	
775.2	6451	lpp1319	1472411	1472971	p	+		unknown	Similar to conserved hypothetical protein	5.2
4293.2	5489	lpp1320	1472984	1473748	p	-		unknown	Similar to conserved hypothetical protein	5.2
5482.2	6152	lpp1321	1473778	1474677	p	-		unknown	Similar to 1-aminocyclopropane-1-carboxylate deaminase	2.2
3909.3	5233	lpp1322	1474889	1476466	p	-		unknown	Class III heat-shock protein HtpG(molecular chaperone)	6
3911.2	5234	lpp1323	1476668	1478539	p	-	htpG			
2382.2	4317	lpp1324	1478651	1478947	m	-		unknown		Similar to DNA-binding protein Fis
2381.2	4316	lpp1325	1479063	1480217	m	-	lpxB	unknown	Similar to lipid-A-disaccharide synthase	1.1
2377.2	4314	lpp1326	1480204	1481166	m	-		unknown	Similar to oxidoreductase	2.1.1
2375.3	4313	lpp1327	1481387	1481962	p	-	rhbB	unknown	Similar to ribonuclease HII	3.1
3913.2	5235	lpp1328	1482074	1483192	m	+	rodA	Rod shape-determining protein rodA	1.7	
3914.3	5236	lpp1329	1483189	1485042	m	+	mrda	penicillin-binding protein 2	1.1	
2239.3	4233	lpp1330	1485268	1486245	p	-		unknown	Similar to hypothetical protein	5.2
2240.2	4234	lpp1331	1486508	1486978	m	-		unknown	Similar to conserved hypothetical protein	5.2
2241.2	4235	lpp1332	1486987	1487325	m	-		unknown	Similar to conserved hypothetical protein	5.2
4384.2	5555	lpp1333	1487430	1488872	m	-		unknown	Similar to proton/peptide symporter family protein	1.2
4385.1	5556	lpp1334	1489095	1490759	p	-	hutU	unknown	Similar to urocanate hydratase (urocanase)	2.2
									(imidazolonepropionate hydrolase)	2.2

Table XIV

4386.2	5557	lpp1335	1490773	1492293	p	-	hutH	unknown	Similar to histidine ammonia-lyase (Histidase)	2.2
4867.2	5869	lpp1336	1492286	1493695	p	-		unknown	Similar to aldehyde dehydrogenase	2.1.1
4868.2	5870	lpp1337	1493707	1494516	p	-		unknown	Similar to short chain dehydrogenase	2.1.1
4869.3	5871	lpp1338	1494513	1494944	p	-	rrhA	unknown	Similar to ribonuclease HI	3.1
5549.2	6183	lpp1339	1494949	1495650	p	-	dnaQ	unknown	Similar to DNA polymerase III, epsilon chain	3.1
5548.1	6182	lpp1340	1495857	1496234	m	-		unknown		6
5546.1	6181	lpp1341	1496526	1496999	p	-		unknown	Some similarity with EnhA protein	5.1
4874.2	5874	lpp1342	1497118	1498521	p	-		unknown		6
4875.1	5875	lpp1343	1498587	1498979	m	-		unknown	Similar to conserved hypothetical protein	5.2
4877.2	5876	lpp1344	1499114	1500199	m	-	trmU	unknown	Similar to tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	3.6
4629.2	5711	lpp1345	1500469	1500897	p	-		unknown		6
4628.2	5710	lpp1346	1500983	1501174	p	-	rpmF	50S ribosomal subunit protein L32		3.7.1
4627.2	5709	lpp1347	1501180	1502208	p	-	plsX	Fatty acid/phospholipid synthesis protein		2.4
4626.1	5708	lpp1348	1502205	1503158	p	-	fabH	3-oxoacyl-[acyl-carrier-protein] synthase III		2.4
4625.2	5707	lpp1349	1503185	1504132	p	-	fabD	Malonyl CoA-acyl carrier protein transacylase		2.4
4803.2	5832	lpp1350	1504144	1504890	p	-	fabG	3-oxoacyl-[acyl-carrier-protein] reductase (3-ketoacyl-acyl carrier protein reductase)		
4804.1	5833	lpp1351	1504975	1505223	p	-	acp	Acyl carrier protein (ACP)		2.4
4805.1	5834	lpp1352	1505243	1506481	p	+	fabF	3-oxoacyl-[acyl-carrier-protein] synthase II (Beta-ketoacyl-ACP synthase II)		2.4
4806.4	5835	lpp1353	1506482	1507480	p	+		unknown	Similar to conserved hypothetical protein	5.2

Table XIV

6042.1	6325	lpp1354	1507480	1508118	p	-	tmk	unknown	Similar to thymidylate kinase	2.3
4958.3	5921	lpp1355	1508115	1509020	p	-		unknown	Similar to DNA polymerase III, delta subunit	3.1
4957.2	5920	lpp1356	1509131	1509487	p	-	pilZ	unknown	Similar to type 4 fimbrial biogenesis protein PilZ	1.8
1346.3	3714	lpp1357	1509547	1510335	p	-	lidH	unknown	Similar to putative deoxyribonuclease belonging to the TatD DNase family	5.2
1345.3	3713	lpp1358	1510447	1511547	p	-		unknown	Similar to conserved hypothetical proteins	5.2
3517.3	4990	lpp1359	1511603	1512895	p	-		unknown	Similar to major facilitator membrane proteins	1.2
1450.2	3776	lpp1360	1513413	1514693	m	-		unknown	similar to multidrug translocase	1.2
3519.1	4991	lpp1361	1514924	1516090	p	-		unknown	Similar to dolichol-phosphate mannosyltransferase	3.8
3520.1	4992	lpp1362	1516178	1517563	m	+		unknown	similar to glycosyl transferase	3.8
3521.2	4993	lpp1363	1517653	1518804	p	-		unknown	similar to putative choline kinase	2.4
3522.1	4994	lpp1364	1518857	1519627	m	-		unknown	Similar to conserved hypothetical proteins	5.2
3524.1	4995	lpp1365	1519873	1520469	p	-		unknown	similar to unknown protein	5.2
3525.1	4996	lpp1366	1520874	1521530	p	-	adk	adenylate kinase		2.3
3527.1	4997	lpp1367	1521539	1521901	p	-		unknown	Similar to thioredoxin proteins	1.4
4228.2	5448	lpp1368	1521861	1523381	m	-	glpD	glycerol-3-phosphate dehydrogenase		2.1.1
4227.1	5447	lpp1369	1523443	1524918	p	-	glpK	Glycerol kinase		2.1.1
1059.2	3546	lpp1370	1525012	1526283	m	-	gltA	citrate synthase		2.1.3
1060.2	3547	lpp1371	1526509	1527390	p	-		unknown	Similar to purine nucleoside phosphorylase proteins	2.3
4226.2	5446	lpp1372	1527474	1530065	p	-	gyrA	DNA gyrase, subunit A, type II topoisomerase		3.4
2395.3	4324	lpp1373	1530058	1531146	p	-	serC	unknown	similar to phosphoserine aminotransferase	2.2
1611.6	3877	lpp1374	1531152	1532453	p	-	aroA	3-phosphoshikimate 1-carboxyvinyltransferase		2.2
5876.3	6290	lpp1375	1532453	1533145	p	-	kcy	Cytidylate kinase		2.3
6039.1	6323	lpp1376	1533211	1534887	p	-	rpsA	30S ribosomal protein S1		3.7.1

Table XIV

5588.2	6203	lpp1377	1535001	1535291	p	+	unknown	Similar to conserved hypothetical protein	5.2
4489.3	5621	lpp1378	1535338	1536507	p	-	unknown	similar to unknown protein	5.2
4488.1	5620	lpp1379	1536771	1537886	p	-	unknown	similar to polysaccharide biosynthesis protein	1.1
4487.1	5619	lpp1380	1537887	1538576	p	-	pyrF	orotidine 5'-phosphate decarboxylase	2.3
1795.3	3998	lpp1381	1538766	1541417	p	-	unknown	6	6
4800.2	5829	lpp1382	1541362	1542141	p	-	unknown	Similar to short-chain dehydrogenase	5.2
4801.1	5830	lpp1383	1542147	1542629	p	+	unknown	6	6
4802.2	5831	lpp1384	1542746	1543282	p	-	unknown	6	6
5587.3	6202	lpp1385	1543279	1544127	p	-	ubiA	Similar to 4-hydroxybenzoate-octaprenyltransferase	2.5
5103.4	6010	lpp1386	1544261	1544659	m	-	unknown	6	6
5104.3	6011	lpp1387	1544739	1546511	m	+	unknown	Similar to oxidase	2.1.1
1794.3	3997	lpp1388	1546565	1547329	m	-	deoC	Similar to 2-deoxyribose-5-phosphate aldolase	2.3
1793.3	3996	lpp1389	1547326	1548165	m	-	xapA	Similar to xanthosine phosphorylase	2.3
5457.1	6141	lpp1390	1548178	1548573	m	-	unknown	Similar to cytidine/deoxycytidine deaminase Cdd	2.3
5003.2	5949	lpp1391	1548612	1549415	m	-	unknown	6	6
5005.3	5950	lpp1392	1549592	1550959	m	+	cpxA	Sensor histidine kinase	1.3
5456.1	6140	lpp1393	1550952	1551632	m	-	cpxR	transcriptional regulatory protein CpxR	3.5.2
3712.2	5126	lpp1394	1551640	1552518	m	-	unknown	Similar to magnesium and cobalt efflux protein CorC	1.2
3711.1	5125	lpp1395	1552490	1552966	m	-	unknown	similar to conserved hypothetical protein	5.2
3710.1	5124	lpp1396	1552963	1553913	m	-	unknown	similar to phosphate starvation-inducible protein PhoH	2.6
3709.1	5122	lpp1397	1554192	1555031	p	-	unknown	similar to TrpH protein	5.2
3708.1	5121	lpp1398	1555028	1555648	p	-	unknown	Similar to putative translation factor	3.5.1
3706.2	5120	lpp1399	1555894	1557108	p	-	trpS	tryptophanyl-tRNA synthetase TrpS	3.7.2

Table XIV

3705.1	5119	lpp1400	1557108	1557899	p	-	scpA	unknown	similar to segregation and condensation protein A	3.4
3703.1	5118	lpp1401	1557901	1558482	p	-	scpB	unknown	similar to segregation and condensation protein B	3.4
3702.1	5117	lpp1402	1558472	1559218	p	-	rluB	unknown	Similar to ribosomal large subunit pseudouridine synthase B (Pseudouridylylate synthase)	3.6
3701.1	5116	lpp1403	1559481	1560239	p	-		Unknown	Similar to transcriptional regulator, LuxR family	3.5.2
3699.3	5114	lpp1404	1560625	1563237	p	-		unknown		6
4242.3	5458	lpp1405	1563333	1564316	p	-		unknown	similar to oxidoreductase	2.1.1
4243.3	5459	lpp1406	1564441	1564890	m	-		unknown	similar to unknown protein	5.2
4244.1	5460	lpp1407	1565108	1565473	p	+		unknown		6
4246.2	5461	lpp1408	1565512	1566363	p	-		unknown	Similar to hydrolases	2.1.1
1323.2	3700	lpp1409	1566490	1567008	p	-		unknown		6
1322.2	3699	lpp1410	1567130	1568515	m	+		unknown	Similar to probable multidrug efflux protein	1.2
1525.3	3820	lpp1411	1568544	1569800	m	+		unknown	Similar to Legionella pneumophila putative phospholipase C	
1528.4	3821	lpp1412	1569921	1571255	p	-	rumA	unknown	Similar to 23S rRNA (Uracil-5-)-methyltransferase Ruma	3.6
1531.3	3825	lpp1413	1571261	1573465	p	-	relA	GTP pyrophosphokinase		2.3
1530.2	3824	lpp1414	1573506	1573871	m	-		unknown	Similar to conserved hypothetical protein	5.2
1529.2	3822	lpp1415	1573930	1575123	p	-		unknown	Similar to putative aminotransferase	2.2
3327.1	4876	lpp1416	1575128	1575937	p	-		unknown	similar to unknown protein	5.2
3328.1	4877	lpp1417	1575927	1577666	p	-	recJ	Single-stranded-DNA-specific exonuclease RecJ		3.3
3331.1	4879	lpp1418	1577745	1578737	p	-		unknown	Similar to tRNA-dihydrouridine synthase A Dusa	3.6
1584.3	3857	lpp1419	1578838	1581528	p	-	secA	Preprotein translocase, secretion protein SecA subunit		1.6
3333.1	4880	lpp1420	1581525	1581929	p	-	mutT	Mutator protein MutT		3.2
3334.2	4881	lpp1421	1582158	1582976	p	+		unknown		6

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5021.3	5957	lpp1422	1583021	1583767	m	-	unknown	similar to conserved hypothetical protein	5.2
5019.1	5955	lpp1423	1584005	1584610	m	-	unknown	Similar to dephospho-CoA kinase	2.5
5018.2	5954	lpp1424	1584582	1585055	m	+	unknown		6
4696.3	5754	lpp1425	1585052	1586650	m	+	Unknown	regulatory protein (EAL domain)	1.3
4694.1	5753	lpp1426	1586789	1588435	p	-	unknown	similar to serine-type D-Ala-D-Ala carboxypeptidase	1.1
4692.5	5752	lpp1427	1588756	1590078	m	-	adenosylmethionine-8-amino-7-oxononanoate aminotransferase		2.5
1598.6	3868	lpp1428	1590151	1591098	p	-	Biotin synthase		2.5
1595.3	3867	lpp1429	1591099	1592241	p	-	8-amino-7-oxononanoate synthase		2.5
1594.2	3866	lpp1430	1592225	1592944	p	-	Biotin biosynthesis protein BioH		2.5
2472.2	4381	lpp1431	1592941	1593579	p	-	Dethiobiotin synthetase		2.5
2473.1	4382	lpp1432	1593714	1594028	p	-	unknown	Similar to conserved hypothetical protein	5.2
2474.1	4383	lpp1433	1594025	1594654	p	-	unknown	Similar to conserved hypothetical protein	5.2
4901.3	5892	lpp1434	1594673	1596454	p	-	aspS	Similar to potassium efflux system kefA	3.7.2
4900.3	5891	lpp1435	1596429	1599380	p	+	unknown		1.2
4376.3	5549	lpp1436	1599343	1600017	p	-	unknown	similar to DNA mismatch repair protein mutH	3.2
4377.4	5550	lpp1437	1600090	1601130	m	-	unknown		6
971.2	6569	lpp1438	1601329	1602165	m	-	Unknown		6
972.3	6570	lpp1439	1602311	1603900	p	-	Unknown	similar to eukaryotic serine threonine protein kinase	3.8
4891.2	5887	lpp1440	1603954	1604703	m	-	Unknown	weak similarity to myosin	6
4889.1	5885	lpp1441	1604962	1605363	m	-	Unknown	similar to unknown protein	5.2
4888.1	5884	lpp1442	1605449	1605970	m	-	unknown	Similar to transcriptional regulator (Lrp family)	3.5.2
4887.3	5883	lpp1443	1606090	1606620	p	-	unknown	Similar to acetyltransferase, GNAT family	2.1.1
5075.4	5994	lpp1444	1606872	1609445	p	-	unknown		6

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5071.2	5993	lpp1445	1609655	1610680	p	-	unknown	similar to adenylate cyclase, family 3	6
4452.2	5596	lpp1446	1610846	1612171	p	-	unknown	Some similarity with eukaryotic proteins	2.3
4453.2	5597	lpp1447	1612347	1613732	p	-	unknown		5.2
4454.4	5598	lpp1448	1613921	1614919	m	-	spectinomycin phosphotransferase		4.2
6036.1	6322	lpp1449	1615172	1615504	p	-	aph	Similar to hypothetical protein	5.1
5584.2	6200	lpp1450	1615585	1616649	m	-	unknown		6.
4993.2	5941	lpp1451	1616882	1617259	m	-	unknown		6
4992.2	5940	lpp1452	1617348	1617641	p	-	unknown		6
4990.3	5939	lpp1453	1618016	1619824	p	-	unknown	Some similarities with sidE protein	5.1
2466.3	4376	lpp1454	1620044	1622725	p	-	unknown	Similar to aminopeptidase N	2.2
4584.3	5683	lpp1455	1622860	1623783	m	-	unknown		6
5559.3	6190	lpp1456	1623870	1624412	m	-	unknown		6
5560.3	6191	lpp1457	1624461	1625102	m	-	unknown	Similar to oxidoreductase	2.1.1
5563.1	6192	lpp1458	1625664	1626128	m	-	unknown	Similar to acetyltransferase	2.1.1
5564.1	6193	lpp1459	1626462	1627886	m	-	lpd	Lipoamide dehydrogenase	2.1.1
908.4	6529	lpp1460	1627975	1629609	m	-	aceF	Pyruvate dehydrogenase (dihydrolipoyltransacetylase component) E2p	2.1.2
907.4	6528	lpp1461	1629667	1632330	m	-	aceE	Pyruvate dehydrogenase (decarboxylase component) E1p	2.1.2
4581.3	5682	lpp1462	1632358	1632747	m	-	unknown	Cystein rich protein	2.1.2
4580.2	5681	lpp1463	1632786	1633538	m	-	unknown	putative membrane protein	5.2
4578.1	5679	lpp1464	1633543	1634715	m	-	unknown	Similar to sodium/hydrogen antiporter family protein	1.2
4577.2	5678	lpp1465	1635034	1635855	m	-	unknown	Similar to rare lipoprotein A RlpA	1.2
4389.2	5560	lpp1466	1635982	1637274	p	+	unknown	Similar to penicillin-binding protein precursor (D-alanyl-D-alanine) carboxypeptidase fraction C	1.1

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4391.1	5561	lpp1467	1637287	1638123	p	-	ala	unknown	Similar to D-alanine aminotransferase	2.2
4392.1	5562	lpp1468	1638127	1638390	p	-		unknown	Similar to conserved hypothetical protein	5.2
4393.1	5563	lpp1469	1638390	1638989	p	-	lssX	Legionella secretion system protein X	member of a putative type I secretion system	1.6
4394.4	5564	lpp1470	1638999	1641035	p	-	lssY	Legionella secretion system protein Y	member of a putative type I secretion system	1.6
5052.4	5978	lpp1471	1641162	1641767	p	-	lssZ	Legionella secretion system protein Z	member of a putative type I secretion system	1.6
5050.2	5977	lpp1472	1641822	1642553	p	-	lssA	Legionella secretion system protein A	member of a putative type I secretion system	1.6
3838.3	5196	lpp1473	1642643	1644799	p	-	lssB	Legionella secretion system protein B	member of a putative type I secretion system	1.6
3840.1	5198	lpp1474	1644803	1645939	p	-	lssD	Legionella secretion system protein D	member of a putative type I secretion system	1.6
3841.2	5199	lpp1475	1646075	1648603	p	-	lssE	unknown	regulatory protein (GGDEF and EAL domains)	1.3
843.2	6484	lpp1476	1648605	1649174	m	-	ppt	unknown	putative pyrimidine phosphoribosyl transferase	2.3
844.2	6485	lpp1477	1649217	1649543	m	-		unknown	Similar to hypothetical protein	5.2
845.4	6486	lpp1478	1649726	1650469	m	-		unknown	Similar to conserved hypothetical protein	5.2
249.4	4394	lpp1479	1650728	1652452	p	-	pilB	pilus assembly protein PilB		1.8
250.1	4400	lpp1480	1652458	1653678	p	-	pilC	pilus assembly protein PilC		1.8
251.2	4406	lpp1481	1653724	1654587	p	-	pilD	Type 4 prepilin-like proteins leader peptide processing enzyme		1.8
252.2	4411	lpp1482	1654601	1655806	m	-		unknown	putative cAMP/cGMP binding protein	4.6
3898.2	5225	lpp1483	1655914	1656507	m	-		unknown		6
3899.2	5226	lpp1484	1656523	1656978	m	-		unknown		6
3901.2	5229	lpp1485	1657112	1657927	p	-		unknown	similar to conserved hypothetical protein	5.2
3902.3	5230	lpp1486	1658047	1659495	m	-	prpD	2-methylcitrate dehydratase		2.1.1
3857.3	5206	lpp1487	1659497	1660615	m	+	prpC	2-methylcitrate synthase		2.1.1

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3855.1	5205	lpp1488	1660831	1661616	m	-	unknown	similar to unknown protein	5.2
1398.2	3744	lpp1489	1661702	1663702	m	-	unknown	Similar to unknown protein	5.2
1399.3	3745	lpp1490	1663695	1665182	m	-	unknown	similar to peptide transport proteins	1.2
3853.2	5204	lpp1491	1665620	1666906	m	-	hemL	Similar to glutamate-1-semialdehyde-2,1-aminomutase	2.5
3851.1	5203	lpp1492	1667294	1667470	p	-	unknown	Similar to rubredoxin protein	1.4
3850.1	5202	lpp1493	1667467	1667889	m	-	unknown	similar to conserved hypothetical protein	5.2
3849.1	5201	lpp1494	1667892	1668623	m	-	unknown	similar to putative transport proteins	1.2
4863.4	5866	lpp1495	1668930	1670201	p	-	pcnB	Poly(A) polymerase (PAP) (Plasmid copy number protein)	3.6
4864.3	5867	lpp1496	1670198	1670623	p	-	folk	Similar to 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	2.5
4865.2	5868	lpp1497	1670678	1671100	p	-	unknown	similar to universal stress protein A	4.1
4987.2	5937	lpp1498	1671177	1672565	m	-	Unknown	UspA	4.6
5255.1	6059	lpp1499	1672570	1673724	m	+	Unknown	Highly similar to GTP-binding proteins	5.2
5254.1	6058	lpp1500	1673749	1674423	m	-	Unknown	Conserved hypothetical protein similar to conserved hypothetical protein	5.2
4712.2	5766	lpp1501	1674441	1675721	m	-	hisS	histidyl-tRNA synthetase	3.7.2
4711.1	5765	lpp1502	1675711	1676280	m	-	Unknown	hypothetical protein	5.2
4710.1	5764	lpp1503	1676255	1677037	m	+	Unknown	similar to fimbrial biogenesis and twitching motility protein (type 4)	1.5
4709.1	5763	lpp1504	1677218	1678366	m	-	Unknown	similar to conserved hypothetical protein	5.2
4706.3	5762	lpp1505	1678387	1678812	m	-	ndk	similar to nucleoside diphosphate kinase	2.3
4705.3	5761	lpp1506	1678947	1679831	m	-	Unknown	conserved hypothetical protein	6.
5253.1	6057	lpp1507	1679905	1680528	p	-	Unknown	conserved hypothetical protein	5.2
5092.3	6003	lpp1508	1680617	1681348	m	-	Unknown	similar to UDP-2,3-diacylglycerolamine hydrolase	6.
5093.3	6004	lpp1509	1681360	1682088	m	-	Unknown		1.1

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5094.2	6005	lpp1510	1682085	1682795	m	-	Unknown	similar to cell division inhibitor MinC (septum placement) Highly similar to acyl-CoA synthetase, long-chain-fatty-acid--CoA ligase	1.7
4525.2	5647	lpp1511	1682852	1684561	p	-	fadD/lidS		2.4
4524.1	5646	lpp1512	1684609	1685325	m	+	unknown	Similar to arginine 3rd transport system periplasmic binding protein	1.2
4523.1	5645	lpp1513	1685486	1686049	m	-	Unknown	similar to unknown protein	5.2
2536.2	4422	lpp1514	1685976	1687298	m	-	pabB	similar to para-aminobenzoate synthase, component I	2.5
2535.2	4421	lpp1515	1687479	1688552	p	-	unknown	similar to pyruvate dehydrogenase, (E1 alpha subunit)	2.1.2
5250.2	6056	lpp1516	1688545	1689519	p	-	Unknown	similar to pyruvate dehydrogenase E1 (beta subunit)	2.1.2
5701.2	6256	lpp1517	1689522	1690634	p	-	Unknown	pyruvate dehydrogenase E2 (dihydrolipoamide acetyltransferase)	2.1.2
3359.2	4890	lpp1518	1690827	1693025	p	+	Unknown	putative transmembrane protein	5.2
1190.4	3626	lpp1519	1693198	1695342	p	+	Unknown	putative Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component	2.1.2
3360.1	4892	lpp1520	1695398	1696108	m	+	Unknown		6
3362.1	4893	lpp1521	1696186	1696911	m	-	Unknown		5.2
3363.2	4894	lpp1522	1697183	1698127	p	-	Unknown	similar to eukaryotic thiamine biosynthesis protein NMT-1	2.3
3365.2	4895	lpp1523	1698130	1699200	p	-	unknown	similar to C.burnetii thiamine biosynthesis oxidoreductase ThiO	2.5
3366.1	4896	lpp1524	1699193	1699396	p	-	this	Similar to thiamine biosynthesis protein ThiS	2.5
702.2	6414	lpp1525	1699399	1700187	p	-	thiG	similar to thiamine biosynthesis protein ThiG	2.5

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2760.1	4543	lpp1549	1725116	1725343	m	-	rpsR	30S ribosomal subunit protein S18	3.7.1
2761.1	4544	lpp1550	1725357	1725695	m	-	rpsF	30S ribosomal protein S6	3.7.1
2763.2	4545	lpp1551	1726004	1726201	p	-		Unknown	similar to carbon storage regulator
2765.2	4546	lpp1552	1726212	1727102	p	+		Unknown	3.5.2
2121.2	4172	lpp1553	1727139	1727873	m	+		unknown	6
1074.3	3556	lpp1554	1727933	1729951	m	-		unknown	5.2
1075.3	3557	lpp1555	1729944	1731263	m	-		unknown	similar to alpha subunit of fatty-acid oxidation complex, 3-hydroxyacyl-CoA dehydrogenase
2120.2	4171	lpp1556	1731428	1732489	m	-		unknown	2.4
402.2	5304	lpp1557	1733202	1734773	m	+		unknown	2.4
401.2	5296	lpp1558	1735049	1736254	m	-		unknown	6
400.1	5289	lpp1559	1736387	1737181	p	-		Unknown	Similar to transposase (ISNCY family)
399.2	5282	lpp1560	1737211	1739634	p	-		Unknown	4.5
2767.1	4547	lpp1561	1739721	1741109	p	-		unknown	6
615.5	6337	lpp1562	1741778	1742419	m	-		Unknown	similar to transposase
5874.2	6289	lpp1563	1742601	1743623	p	-		Unknown	Similar to transposase (IS21 family)
6217.2	6352	lpp1564	1743620	1744414	p	-		Unknown	Similar to transposase (IS21 family)
5328.1	6088	lpp1565	1744456	1744953	m	-		Unknown	Similar to transposase (ISL3 family)
4209.2	5437	lpp1566	1744987	1746135	m	-		Unknown	Similar to transposase (ISL3 family)
2298.2	4262	lpp1567	1746200	1747495	m	-		Unknown	Some similarities to eukaryotic proteins
1035.3	3529	lpp1568	1747969	1749393	p	-	plaB	phospholipase	6.
4473.4	5610	lpp1569	1749465	1750142	m	-		Unknown	2.4
4474.1	5611	lpp1570	1750144	1750518	m	-		Unknown	similar to hypothetical proteins
4475.1	5612	lpp1571	1750710	1751390	p	-		Unknown	Similar to hypothetical proteins
									similar to conserved hypothetical proteins

Table XIV

4477.2	5613	lpp1572	1751628	1753943	p	-	Unknown	similar to phosphoenolpyruvate carboxylase	2.1.2
4479.2	5614	lpp1573	1754096	1754578	p	-	Unknown	similar to MutT/nudix family protein	3.2
4480.4	5616	lpp1574	1754629	1755882	m	-	proA gamma-glutamyl phosphate reductase		
5090.2	6002	lpp1575	1755891	1756961	m	-	proB glutamate 5-kinase		2.2
5088.2	6000	lpp1576	1757251	1757676	m	-	Unknown	Similar to acetyltransferase, GNAT family	2.1.1
5660.1	6239	lpp1577	1757883	1758863	p	-	Unknown	similar to hypothetical proteins	5.2
5056.3	5980	lpp1578	1759030	1759365	p	-	unknown	similar to unknown protein	5.2
5058.2	5981	lpp1579	1759597	1759836	m	-	Unknown	Similar to transposase (IS5 family)	4.5
5059.3	5982	lpp1580	1759829	1760140	m	-	Unknown	Similar to transposase (IS5 family)	4.5
602.4	6320	lpp1581	1760325	1761272	m	-	Unknown	Similar to transcription regulators (MerR Family)	3.5.2
604.3	6324	lpp1582	1761480	1762229	m	-	Unknown	similar to transcription regulator (MerR family)	3.5.2
4623.2	5706	lpp1583	1762295	1762822	m	-	Unknown	Similar to acetyltransferase, GNAT family	2.1.1
5054.2	5979	lpp1584	1762819	1763775	m	-	Unknown	similar to hypothetical proteins	5.2
4004.2	5293	lpp1585	1763779	1765560	m	-	unknown	similar to multidrug resistance ABC transporter ATP-binding protein	1.2
4003.1	5292	lpp1586	1765553	1767013	m	-	Unknown	similar to ATPase components of ABC transporters with duplicated ATPase domains	1.2
1223.2	3643	lpp1587	1767380	1768255	p	-	Unknown	Weakly similar to cytochrome C family proteins	1.4
1224.2	3644	lpp1588	1768315	1769115	m	+	Unknown	Similar to class-D beta-lactamase	4.2
4002.2	5291	lpp1589	1769165	1771075	m	+	Unknown	similar to Cell division protein FtsI/penicillin-binding protein 2	1.7
4000.2	5290	lpp1590	1771075	1771515	m	-	Unknown	Similar to transcriptional regulator (MarR family)	3.5.2
4307.2	5499	lpp1591	1771686	1773005	m	-	Unknown		6
2261.3	4243	lpp1592	1773175	1773933	m	-	Unknown		6.
1098.3	3571	lpp1593	1774067	1775083	m	-	Unknown	similar to conserved hypothetical proteins	5.2

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1099.2	3572	lpp1594	1775376	1776359	p	-	unknown	similar to unknown protein	5.2
4305.2	5498	lpp1595	1776384	1776779	m	-	Unknown	6	
5582.4	6199	lpp1596	1777014	1779221	m	-	Unknown	putative copper efflux ATPase	1.2
4088.2	5351	lpp1597	1779397	1780290	p	-	Unknown	Similar to unknown protein	5.1
4087.2	5350	lpp1598	1780384	1781658	m	-	Unknown	similar to conserved hypothetical proteins	5.2
1111.3	3581	lpp1599	1781652	1782488	m	-	Unknown	similar to conserved hypothetical protein	5.2
1109.3	3579	lpp1600	1782473	1783453	m	-	Unknown	similar to 3-beta hydroxysteroid dehydrogenase/isomerase	2.4
1107.2	3578	lpp1601	1783455	1784438	m	-	unknown	Similar to 3-oxoacyl-[acyl-carrier-protein] synthase III	2.4
4084.3	5349	lpp1602	1784588	1785754	p	-	Unknown	similar to glycosyl transferase	1.1
4083.4	5348	lpp1603	1785751	1786407	p	-	unknown	6	
1577.5	3851	lpp1604	1786587	1789487	m	-	unknown	Similar to oxidoreductase proteins	2.1.1
4332.1	5515	lpp1605	1789642	1790181	p	-	Unknown	similar to hypothetical proteins	5.2
4333.1	5516	lpp1606	1790235	1791083	p	-	unknown	similar to acetyltransferase, GNAT family	2.1.1
4334.1	5517	lpp1607	1791087	1791977	p	-	unknown	similar to unknown protein	5.2
4336.2	5518	lpp1608	1792193	1793407	p	-	Unknown	similar to permease of the major facilitator superfamily	1.2
4632.1	5712	lpp1609	1793420	1794679	m	-	Unknown	6	
4633.2	5713	lpp1610	1794827	1795384	p	-	Unknown	similar to conserved hypothetical proteins	5.2
4634.2	5714	lpp1611	1795402	1797372	m	-	unknown	similar to acylaminoacyl-peptidase proteins	2.2
4181.1	5422	lpp1612b	1797582	1798151	m	-	unknown	C-terminal part of L. pneumophila sidB protein	6
2354.2	4296	lpp1612a	1798221	1798835	m	-	unknown	Similar to N-terminal part of sidB protein	6
1748.3	3965	lpp1613	1799215	1800489	m	-	unknown	similar to threonine synthase ThrC	2.2
1749.2	3966	lpp1614	1800656	1801420	m	+	Unknown	similar to putative outer membrane proteins	5.2
4179.2	5420	lpp1615	1801721	1803745	m	-	Unknown	Some similarities with L. pneumophila SidE protein	5.1

Table XIV

1295.1	3687	lpp1616	1803892	1804467	m	+	Unknown	similar to conserved hypothetical proteins	5.2
1294.2	3686	lpp1617	1804467	1804997	m	-	Unknown	similar to Cytochrome B561	1.4
1293.4	3685	lpp1618	1805001	1805594	m	+	Unknown	similar to conserved hypothetical proteins	5.2
4337.3	5519	lpp1619	1805622	1805879	m	+	Unknown	putative secreted protein	5.2
4338.3	5520	lpp1620	1806001	1806897	m	-	Unknown	similar to myo-inositol catabolism protein ioIE	2.1.1
4339.1	5521	lpp1621	1806900	1808771	m	-	Unknown	similar to malonic semialdehyde oxidative decarboxylase	2.1.1
4340.2	5523	lpp1622	1808810	1810696	m	-	Unknown	Bifunctional protein similar to IoIC (sugar kinase) and IoIB	
5386.1	6108	lpp1623	1810704	1811654	m	-	Unknown	similar to myo-inositol 2-dehydrogenase	2.1.1
4786.2	5821	lpp1624	1811711	1813126	m	+	Unknown	similar to sugar-proton symporter	1.2
4785.1	5820	lpp1625	1813578	1814693	m	-	Unknown		6.
4751.2	5795	lpp1626	1814891	1816564	m	-	Unknown	similar to metalloprotease	2.2
1516.3	3815	lpp1627	1816606	1817529	m	-	Unknown	similar to hypothetical proteins	5.2
1515.2	3814	lpp1628	1817711	1818478	p	-	Unknown	similar to dimethylarginine dimethylaminohydrolase	2.2
1513.4	3813	lpp1629	1818457	1819794	p	+	Unknown	similar to amino acid transporter	1.2
5022.2	5958	lpp1630	1819930	1820967	p	-	Unknown	similar to hypothetical proteins	5.2
3988.3	5280	lpp1631	1821106	1822587	p	-	Unknown		6.
3986.1	5279	lpp1632	1822681	1823799	m	-	Unknown	similar to conserved hypothetical proteins	5.2
3985.1	5278	lpp1633	1823960	1824556	p	-	Unknown	similar to putative transport proteins, MFS family	1.2
856.2	6491	lpp1634	1824720	1825232	p	-	Unknown		6.
857.2	6492	lpp1635	1825291	1827618	m	+	Unknown		2.2
4908.3	5894	lpp1636	1827781	1833546	p	+	Unknown	similar to putative membrane proteins	5.2
1671.3	3917	lpp1637	1833794	1835197	m	+	Unknown		6.
3995.5	5286	lpp1638	1835358	1836725	m	-	Unknown		6.
3994.5	5285	lpp1639	1836897	1837721	m	-	Unknown		6.
3993.2	5284	lpp1640	1837986	1838543	p	-	Unknown		6.
887.4	6511	lpp1641	1838869	1840971	m	-	Unknown		5.1

Table XIV

5711.2	6258	lpp1642	1841397	1842287	p	-	Unknown	6
5193.2	6033	lpp1643	1842391	1844508	p	-	unknown	5.1
3938.3	5251	lpp1644	1844505	1845083	m	-	Phosphoribosylglycinamide formyltransferase	2.3
3937.3	5250	lpp1645	1845080	1846399	m	-	Phosphoribosylamine- glycine ligase	2.3
2272.3	4250	lpp1646	1846396	1847895	m	-	Amidophosphoribosyltransf erase	2.3
2274.2	4251	lpp1647	1847918	1848856	m	-	Phosphoribosylamidoimidaz ole-succinocarboxamide synthase	2.3
3936.2	5249	lpp1648	1848879	1850138	m	-	Phosphoribosylformylglycin amidase synthase I (FGAM synthase I)	2.3
1972.3	4101	lpp1649	1850138	1851181	m	-	Phosphoribosylformylglycin amidase synthase I (FGAM synthase I)	2.3
278.4	4557	lpp1650	1851181	1853523	m	-	Phosphoribosylformylglycin amidase synthase II (FGAM synthase II)	2.3
277.1	4549	lpp1651	1853676	1854389	m	-	Unknown	2.3
276.1	4542	lpp1652	1854460	1854654	m	+	Unknown	5.2
1754.3	3969	lpp1653	1854956	1856305	m	+	unknown	6.
1755.3	3970	lpp1654	1856433	1856750	m	+	Unknown	3.9
1756.4	3971	lpp1655	1856847	1857698	m	-	Unknown	6
2669.2	4489	lpp1656	1858242	1859444	m	-	Unknown	2.1.1
2670.1	4491	lpp1657	1859481	1860725	m	-	Unknown	6
2671.1	4492	lpp1658	1860909	1861535	p	-	Unknown	1.5
2674.1	4493	lpp1659	1861620	1864295	p	-	Aconitate hydratase	6
2677.2	4494	lpp1660	1864560	1865954	p	+	unknown	2.1.3
							similar to amino acid antiporter	1.2
							similar to oxidoreductase, short- chain dehydrogenase/reductase family	
							some similarity with flagellar hook- length control protein FliK	

Table XIV

847.4	6487	lpp1661	1866148	1869300	m	-	putA	unknown	similar to bifunctional PutA protein (proline dehydrogenase/ delta-1- pyrroline-5-carboxylate dehydrogenase)	2.2
2680.1	4496	lpp1662	1869857	1870534	p	+		unknown	conserved hypothetical protein similar to activator of	5.2
1708.4	3941	lpp1663	1870966	1871331	p	-		Unknown	osmoprotectant transporter ProP (N-terminal part)	4.1
1709.1	3942	lpp1664	1871359	1872051	m	-	ubiG	3-demethylubiquinone-9 3- methyltransferase		2.5
1711.2	3943	lpp1665	1872038	1872757	m	-		unknown	similar to Uracil-DNA glycosylase	3.2
2292.2	4258	lpp1666	1873027	1874706	p	-		unknown		6.
2682.1	4497	lpp1667	1874842	1876482	p	-		Unknown		6.
1036.4	3530	lpp1668	1876569	1877825	m	-	umuC	Unknown	similar to error-prone repair protein	3.2
1037.1	3531	lpp1669	1877825	1878241	m	-	umuD	Unknown	similar to error-prone repair: SOS- response transcriptional repressors (LexA homologs, RecA-mediated autopeptidases)	3.2
1039.2	3532	lpp1670	1878515	1879738	p	-		Unknown	similar to carboxypeptidase G2 and to acetylornithine deacetylase/Succinyl- diaminopimelate desuccinylase	2.2
2144.4	4187	lpp1671	1879738	1880778	p	-	astA	arginine N- succinyltransferase, beta chain		2.2
2683.4	4498	lpp1672	1880792	1882279	p	-	astD	Succinylglutamic semialdehyde dehydrogenase		2.2
5195.2	6034	lpp1673	1882285	1883631	p	-	astB	succinylarginine dihydrolase		2.2
2685.2	4499	lpp1674	1883643	1884368	p	-		unknown	similar to unknown proteins	5.2
4732.3	5781	lpp1675	1884446	1884811	m	+		Unknown	Weakly similar to cytochrome c5	1.4
1743.4	3962	lpp1676	1885233	1885790	m	-	rrf	Ribosome recycling factor		3.7.5

Table XIV

1742.3	3961	lpp1677	1885780	1886523	m	-	pyrH	Uridylate kinase (UK) (Uridine monophosphate kinase)		2.3
4733.2	5782	lpp1678	1886520	1887398	m	-	tsf	Elongation factor Ts (EF- Ts)		3.7.4
4999.2	5944	lpp1679	1887464	1888228	m	-	rpsB	30S ribosomal protein S2		3.7.1
5000.3	5947	lpp1680	1888562	1888972	p	+		Unknown	16 kD immunogenic protein	5.1
5001.1	5948	lpp1681	1889494	1889940	p	-		Unknown		6.
5307.3	6075	lpp1682	1890005	1891693	m	-		Unknown		6.
3991.3	5283	lpp1683	1892084	1893769	m	-		Unknown	ankyrin repeat protein similar to methionine aminopeptidase, type I	6.
837.2	6479	lpp1684	1893865	1894629	p	-		Unknown		2.2
835.2	6478	lpp1685	1894616	1897201	p	-	glnD	unknown	similar to PII uridylyl-transferase	3.8
3989.1	5281	lpp1686	1897223	1897672	m	-		Unknown	similar to hypothetical proteins	5.2
1210.2	3636	lpp1687	1897663	1899240	m	-	guaA	Unknown	similar to GMP synthetase (glutamine-hydrolyzing)	2.3
1209.2	3634	lpp1688	1899243	1900715	m	-	guaB	Unknown	similar to IMP dehydrogenase/GMP reductase	2.3
5309.1	6076	lpp1689	1900924	1901754	p	-	minD	Septum site-determining protein (Cell division inhibitor)		1.7
2514.3	4408	lpp1690	1901751	1902020	p	-	minE	Septum formation topological specificity factor		1.7
893.4	6515	lpp1691	1902336	1904822	m	+		Unknown	similar to acyl-CoA dehydrogenase	2.4
4472.2	5609	lpp1692	1904915	1905700	m	-		Unknown	similar to putative hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	2.1.1
4744.3	5790	lpp1693	1905697	1906605	m	-		Unknown	similar to hypothetical proteins	5.2
1503.4	3806	lpp1694	1906565	1907656	m	-		Unknown	similar to sn-glycerol-3-phosphate transport ATP-binding protein	1.2
1501.3	3805	lpp1695	1907656	1908483	m	+		Unknown	similar to glycerol-3-phosphate ABC transporter, permease component	1.2

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2388.3	4320	lpp1696	1908480	1909358	m	-	Unknown	similar to glycerol-3-phosphate ABC transporter, permease components	1.2
2387.3	4319	lpp1697	1909478	1910479	p	-	Unknown	similar to quinone oxidoreductase (NADPH:quinone reductase)	1.4
1144.3	3600	lpp1698	1910653	1911936	m	-	clcA	similar to Voltage-gated ClC-type chloride channel	1.2
1145.3	3601	lpp1699	1911929	1914085	m	-	trpE		2.2
5311.1	6078	lpp1700	1914350	1914646	p	-	gatC	Anthranilate synthase Glutamyl-tRNA(Gln) amidotransferase (subunit C)	3.7.2
4094.2	5354	lpp1701	1914649	1916100	p	-	gatA	Glutamyl-tRNA(Gln) amidotransferase (subunit A)	
4093.1	5353	lpp1702	1916104	1917537	p	-	gatB	Glutamyl-tRNA(Gln) amidotransferase (subunit B)	
2343.2	4287	lpp1703	1917751	1918740	p	-	Unknown		6.
2344.4	4288	lpp1704	1918909	1921185	p	-	Unknown	similar to Adenylate cyclase 1(ATP pyrophosphate-lyase 1; Adenylylcyclase 1)	2.3
5478.2	6148	lpp1705	1921225	1921686	p	+	Unknown		6
1115.4	3582	lpp1706	1921706	1922494	p	+	Unknown		6
5477.1	6147	lpp1707	1923066	1923353	m	-	Unknown	similar to DNA-binding protein fis	3.5.2
5476.1	6146	lpp1708	1923748	1924116	m	-	Unknown	similar to HesB/YadR/YfhF family proteins	5.2
3556.2	5018	lpp1709	1924121	1924504	m	-	unknown	similar to iron-sulphur cluster proteins NifU	2.5
3557.1	5019	lpp1710	1924501	1925664	m	-	IscS	similar cysteine desulfurase	3.8
427.3	5475	lpp1711	1925639	1926412	m	-	Unknown	similar to putative tRNA/rRNA methyltransferase	3.6
428.1	5480	lpp1712	1926528	1927313	p	-	Unknown	similar to inositol-1- monophosphatase	2.1.1
429.2	5487	lpp1713	1927426	1928382	m	-	Unknown	similar to putative signal peptide peptidases	1.6
2092.2	4159	lpp1714	1928471	1931047	p	-	clpB	endopeptidase Clp ATP- binding chain B (ClpB)	4.1
3559.2	5020	lpp1715	1931139	1932452	m	-	unknown		6.

Table XIV

1886.2	4052	lpp1716	1932465	1933073	m	-	Unknown	6.	similar to UDP-N-acetylmutamate: L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase
1885.3	4051	lpp1717	1933405	1934772	m	+	mpl	Unknown	
4649.2	5723	lpp1718	1934774	1935394	m	-	unknown	1.1	hypothetical gene
4650.4	5725	lpp1719	1935447	1939268	m	+	unknown	6	similar to unknown protein
4262.2	5471	lpp1720	1939258	1939713	m	-	fliJ	1.5	similar to flagellar protein FliJ
2550.2	4429	lpp1721	1939710	1941059	m	-	fliI	1.5	flagellum-specific ATP synthase FliI
2551.2	4430	lpp1722	1941062	1941700	m	-	fliH	1.5	Polar flagellar assembly protein FliH
2553.3	4431	lpp1723	1941842	1942831	m	-	fliG	1.5	Flagellar motor switch protein
4259.3	5469	lpp1724	1942834	1944468	m	-	fliF	1.5	Flagellar M-ring protein
3675.1	5099	lpp1725	1944641	1944955	m	-	fliE	1.5	Flagellar hook-basal body complex protein
3676.2	5100	lpp1726	1944970	1946283	m	-	fliR	3.5.2	similar to two-component response regulator
3679.3	5101	lpp1727	1946307	1947338	m	-	fliS	3.5.2	similar to sensor histidine kinase
561.3	6215	lpp1728	1947637	1948941	m	-		5.2	conserved hypothetical protein
562.1	6217	lpp1729	1948957	1949565	m	+		3.9	similar to periplasmic chaperone LolA
564.2	6228	lpp1730	1949568	1951952	m	-	ftsK	1.7	similar to cell division protein FtsK
3680.1	5103	lpp1731	1952025	1952975	p	+	trxB	1.4	Thioredoxin reductase
3681.1	5104	lpp1732	1952978	1953646	p	-	aat	3.8	similar to leucyl/phenylalanyl-tRNA- protein transferase
3682.1	5105	lpp1733	1953710	1954081	p	-		5.2	similar to rhodanese domain protein
3683.2	5106	lpp1734	1954213	1954434	p	-	infA	3.5.1	Translation initiation factor IF-1
5295.1	6072	lpp1735	1954598	1955956	m	-	pmbA	1.2	unknown
2448.3	4364	lpp1736	1956002	1956778	p	+		5.2	Similar to conserved hypothetical protein
2447.3	4363	lpp1737	1957028	1957978	p	-		6.	Unknown

Table XIV

2445.4	4362	lpp1738	1958250	1961078	p	-	rir1	unknown	similar to ribonucleoside-diphosphate reductase, alpha subunit	2.3
4797.1	5826	lpp1739	1961092	1962195	p	-	rir2	unknown	Similar to ribonucleoside-diphosphate reductase, beta subunit	2.3
4796.1	5825	lpp1740	1962509	1962991	p	+		unknown		6
4005.2	5294	lpp1741	1963078	1964568	m	-	lysS	unknown	Highly similar to lysyl-tRNA synthetase	3.7.2
4009.1	5295	lpp1742	1964565	1965572	m	-	prfB	unknown	Highly similar to peptide chain release factor 2	3.5.4
4010.1	5297	lpp1743	1965732	1966133	m	-		Unknown	similar to hypothetical proteins	5.2
4012.1	5298	lpp1744	1966130	1966951	m	-	motB	unknown	Similar to chemotaxis MotB protein	1.5
4013.1	5299	lpp1745	1966908	1967681	m	-	motA	flagellar motor protein		1.5
4014.1	5300	lpp1746	1967691	1968407	m	-	fliA	sigma factor 28		3.5.1
4015.1	5301	lpp1747	1968504	1969373	m	-	fliN	unknown	similar to flagellar synthesis regulator	1.5
4016.1	5302	lpp1748	1969360	1970499	m	-	fliH	Flagellar biosynthesis protein FliH		1.5
4017.4	5303	lpp1749	1970540	1972618	m	-	fliA	Flagellar biosynthesis protein fliA		1.5
5361.2	6099	lpp1750	1972615	1973763	m	-	fliB	Flagellar biosynthetic protein FliB		1.5
2593.3	4452	lpp1751	1973763	1974533	m	-	fliR	Flagellar biosynthetic protein fliR		1.5
5026.1	5959	lpp1752	1974537	1974806	m	+	fliQ	Flagellar biosynthetic protein FliQ		1.5
2595.4	4453	lpp1753	1974815	1975564	m	+	fliP	Flagellar biosynthetic protein FliP		1.5
5359.2	6097	lpp1754	1975565	1975975	m	-	fliO	Flagellar protein fliO		1.5
4526.3	5648	lpp1755	1975972	1976307	m	-	fliN	Flagellar motor switch protein FliN		1.5
1585.2	3858	lpp1756	1976317	1977378	m	-	fliM	Flagellar motor switch protein FliM		1.5
1586.2	3859	lpp1757	1977823	1978062	m	+		Unknown		6.
1587.4	3860	lpp1758	1978181	1979476	p	-		Unknown	similar to oxidoreductase	2.1.1
4275.2	5478	lpp1759	1979473	1980195	p	+		Unknown	similar to hypothetical oxidoreductase	2.1.1

Table XIV

5278.3	6066	lpp1783	2014105	2014887	m	-	unknown		6
5277.3	6065	lpp1784	2014908	2015909	m	-	Dihydroorotate dehydrogenase		2.3
3070.2	4723	lpp1785	2016195	2017193	m	+	unknown	Predicted transmembrane protein	
3069.1	4721	lpp1786	2017242	2017928	m	-	unknown	Similar to conserved hypothetical protein	6
3068.1	4720	lpp1787	2018254	2019423	p	-	unknown	Similar to acyl-CoA dehydrogenase	5.2
2538.2	4423	lpp1788	2019435	2020619	p	-	unknown	Similar to acetyl-CoA acetyltransferase	2.4
3067.1	4719	lpp1789	2020751	2021071	p	+	Unknown	hypothetical gene	6
568.2	6245	lpp1790	2021081	2022688	p	-	unknown	similar to Acetyl/propionyl-CoA carboxylase, beta subunit	2.2
569.2	6250	lpp1791	2022672	2023502	p	-	Unknown	similar to enoyl-CoA hydratase/isomerase	2.2
571.2	6257	lpp1792	2023495	2025459	p	-	Unknown	similar to Acetyl/propionyl-CoA carboxylase, alpha subunit	2.2
2007.1	4115	lpp1793	2025470	2026378	p	-	unknown	Similar to hydroxymethylglutaryl-CoA lyase	2.2
1127.3	3591	lpp1794	2026535	2028475	p	-	unknown	Similar to acetyl-coenzyme A synthetase	2.1.1
3065.1	4718	lpp1795	2028635	2029051	m	+	unknown	similar to unknown proteins	5.2
3063.2	4717	lpp1796	2029504	2030529	p	-	unknown	Similar to ABC transporter, ATP-binding protein	1.2
3061.2	4716	lpp1797	2030507	2031154	p	-	unknown	Similar to ABC transporter permease protein	1.2
3059.2	4714	lpp1798	2031167	2031946	p	+	Unknown	29 kDa immunogenic protein	4.6
1058.3	3545	lpp1799	2032026	2033444	p	-	unknown	Some similarity with eukaryotic protein	6
1056.1	3544	lpp1800	2033770	2033937	p	-	unknown		6
1055.1	3543	lpp1801	2033934	2034665	m	-	unknown	Similar to conserved hypothetical protein	5.2
1053.2	3542	lpp1802	2034668	2035198	m	-	unknown	Similar to phosphatase	2.6
1713.2	3944	lpp1803	2035204	2037270	m	-	glyS	glycyl-tRNA synthetase beta chain	3.7.2
1714.4	3945	lpp1804	2037260	2038165	m	-	glyQ	glycyl-tRNA synthetase alpha chain	3.7.2

Table XIV

1797.4	3999	lpp1805	2038400	2039185	m	+	unknown	Similar to outer membrane protein	1.1
1800.5	4002	lpp1806	2039393	2041558	m	-	uvrD		3.2
4419.3	5578	lpp1807	2041779	2042738	p	-		similar to proline iminopeptidase	2.2
5470.2	6144	lpp1808	2042732	2043169	p	-		similar to D-tyrosyl-tRNA(Tyr) deacylase	2.2
1260.4	3663	lpp1809	2043387	2044169	p	+		conserved lipoprotein	5.2
1258.1	3661	lpp1810	2044278	2045237	m	-	gshB	glutathione synthetase	4.1
1257.6	3660	lpp1811	2045237	2046532	m	-		similar to unknown proteins	5.2
6322.1	6369	lpp1812	2046691	2046984	m	-		Similar to conserved hypothetical protein	5.2
6320.1	6368	lpp1813	2047010	2048095	m	-		Similar to transposase (IS4 family)	4.5
382.6	5185	lpp1814	2048181	2048459	p	-		hypothetical gene	6
5097.1	6006	lpp1815	2048548	2049444	p	+		putative membrane protein, similar to permease of the drug/metabolite transporter (DMT) superfamily	1.2
5098.2	6007	lpp1816	2049448	2049729	p	-			6.
3536.2	5003	lpp1817	2049767	2050066	p	-		hypothetical protein (rhodanese domain)	5.2
3535.5	5002	lpp1818	2050100	2050762	m	-			6.
3534.2	5001	lpp1819	2051132	2052769	p	+		similar to putative alkaline phosphatase	2.6
3533.1	5000	lpp1820	2052762	2053460	p	+	udk		2.3
1487.3	3797	lpp1821	2053556	2054362	p	-	fabI	similar to Enoyl-[acyl-carrier-protein] reductase	2.4
3532.1	4999	lpp1822	2054814	2058023	m	-			6
3530.1	4998	lpp1823	2058161	2058787	p	-			5.1
1787.4	3992	lpp1824	2059070	2062204	m	-		Some similarity with eukaryotic proteins	5.2
4512.4	5638	lpp1825	2062777	2064651	m	-		similar to peptidyl-prolyl cis-trans isomerase D	3.9
4511.1	5637	lpp1826	2064909	2065187	m	-	hubB	similar to DNA-binding protein HU-beta	3.4
4510.1	5636	lpp1827	2065316	2067766	m	-	lon	similar to ATP-dependent protease La	4.1

Table XIV

3741.1	5140	lpp1848	2092904	2094121	p	-	Unknown	Some similarity with eukaryotic proteins	5.2
3743.1	5141	lpp1849	2094443	2094757	p	+	Unknown		6.
3744.2	5142	lpp1850	2094922	2096031	m	+	Unknown		6
6318.1	6366	lpp1851	2096462	2097547	p	-	Unknown	Similar to transposase (IS4 family)	4.5
4220.2	5443	lpp1852	2097573	2097866	p	-	unknown	similar to conserved hypothetical protein	5.2
4221.3	5444	lpp1853	2098044	2098319	m	-	unknown	Similar to acylphosphatase	2.4
4222.3	5445	lpp1854	2098476	2098829	p	-	unknown	Q-rich protein	6
1670.3	3916	lpp1855	2099011	2100342	m	-	unknown		6
1669.3	3915	lpp1856	2100571	2101536	p	-	unknown	Similar to esterase/lipase	2.4
1673.5	3918	lpp1857	2101600	2103261	m	-	unknown		6
1675.3	3919	lpp1858	2103397	2103699	p	-	unknown	Similar to hypothetical protein	5.2
5174.2	6025	lpp1859	2103753	2104172	p	+	unknown	signal peptide predicted	6
4080.2	5346	lpp1860	2104182	2105462	m	+	unknown	Similar to major facilitator family transporter (MFS)	1.2
4078.1	5344	lpp1861	2105939	2107219	p	-	unknown	similar to chloride channel protein	1.2
1735.1	3955	lpp1862	2107418	2107564	m	-	unknown		6
1737.2	3956	lpp1863	2107802	2108908	m	-	unknown	Similar to hypothetical protein	5.2
4076.1	5343	lpp1864	2109110	2109613	p	-	unknown		6
4075.3	5342	lpp1865	2109877	2110356	p	-	unknown	Similar to hypothetical protein	5.2
3760.3	5151	lpp1866	2110376	2112181	p	+	unknown	Similar to glutathione-regulated potassium-efflux system protein KefC (K(+)/H(+)-antiporter)	1.2
3763.1	5152	lpp1867	2112357	2112968	m	-	unknown	Similar to hypothetical protein	5.2
3764.3	5153	lpp1868	2113061	2113363	m	-	unknown		6
2427.4	4348	lpp1869	2113758	2114093	p	-	Unknown	similar to unknown protein	5.2
2428.2	4349	lpp1870	2114117	2114389	m	-	Unknown	Similar to transposase (IS5 family)	4.5
2429.2	4350	lpp1871	2114625	2115539	p	-	unknown	Similar to MoxR-like ATPases, putative regulator	3.5.2
3765.1	5154	lpp1872	2115536	2116486	p	-	unknown	Similar to conserved hypothetical protein	5.2
5173.1	6024	lpp1873	2116486	2118474	p	-	unknown	Similar to unknown protein	5.2

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3607.2	5051	lpp1874	2118556	2119743	p	-	unknown	similar to conserved hypothetical protein	5.2
3608.1	5052	lpp1875	2119851	2120177	p	-	unknown		6
1066.2	3550	lpp1876	2120613	2121515	p	-	unknown	similar to hypothetical protein	5.2
1067.1	3551	lpp1877	2121681	2121923	m	-	unknown		6
1069.2	3552	lpp1878	2122150	2123079	m	-	unknown	Similar to conserved hypothetical protein	5.2
2108.2	4165	lpp1879	2123354	2124268	m	-	unknown	similar to hypothetical transporter	1.2
1278.2	3675	lpp1880	2124526	2125665	p	+	unknown	similar to eukaryotic ectonucleoside triphosphate diphosphohydrolase (apyrase)	2.3
1279.3	3676	lpp1881	2125670	2126203	m	-	unknown	Similar to conserved hypothetical protein	5.2
2905.2	4614	lpp1882	2126214	2128019	m	-	unknown		6
2906.2	4615	lpp1883	2128346	2128951	m	-	gst	glutathione S-transferase	4.1
2908.2	4616	lpp1884	2129148	2130143	m	-	unknown		6
2909.1	4617	lpp1885	2130184	2131446	m	-	unknown	Similar to D-alanyl-D-alanine carboxypeptidase	1.1
2910.1	4619	lpp1886	2131693	2133105	m	-	gltx	Glutamyl-tRNA synthetase, catalytic subunit	3.7.2
994.2	6585	lpp1887	2133204	2135936	p	+	gacS/letS	Legionella transmission sensor LetS	1.3
993.2	6584	lpp1888	2136034	2137278	p	-	pfp	similar to PPi dependent phosphofructokinase	2.1.2
2170.1	4206	lpp1889	2137275	2137688	m	+	unknown	similar to type IV pilin PilA	1.8
2169.2	4205	lpp1890	2137882	2138292	m	+	unknown	similar to type IV pilin PilA	1.8
2911.3	4620	lpp1891	2138595	2138912	p	-	unknown	Similar to BolA protein	4.1
1142.4	3599	lpp1892	2138987	2140408	p	+	unknown	Similar to amino acid antiporter	1.2
1658.2	3907	lpp1893	2140514	2141944	m	-	unknown	weakly similar to endoglucanase	2.1.1
1657.1	3906	lpp1894	2142192	2142944	m	-	kdsB	3-deoxy-manno-octulosonate cytidyltransferase	1.1
1655.2	3905	lpp1895	2142941	2143120	m	-	unknown	Similar to hypothetical protein	5.2
2914.1	4621	lpp1896	2143113	2143784	m	-	unknown	Similar to conserved hypothetical protein	5.2

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389.3	5220	lpp1897	2143762	2145720	m	-	unknown	Similar to ATP-dependent DNA helicase	3.2
390.2	5228	lpp1898	2145708	2146043	m	-	unknown	Similar to ferredoxin	1.4
2915.2	4622	lpp1899	2146325	2149117	p	-	unknown		6
790.3	6457	lpp1900	2149421	2152066	p	-	unknown		6
4604.3	5697	lpp1901	2152142	2152699	p	-	unknown	Similar to conserved hypothetical protein	5.2
4930.2	5908	lpp1902	2152775	2153044	p	-	unknown	Similar to conserved hypothetical protein	5.2
4929.2	5906	lpp1903	2153056	2153982	p	-	unknown	Similar to conserved hypothetical protein	5.2
4927.1	5905	lpp1904	2154197	2154922	p	-	unknown		6
413.5	5379	lpp1905	2155355	2157721	p	-	unknown	ankyrin repeat protein	6
415.2	5397	lpp1906	2158068	2159177	m	-	Unknown	similar to N-terminal part of putative transposase (IS91 family)	4.5
417.3	5412	lpp1907	2159832	2160641	p	-	Unknown		6.
6314.1	6365	lpp1908	2160593	2160793	p	-	Unknown		6.
2026.1	4124	lpp1909	2160742	2161014	m	-	unknown		6
2027.2	4125	lpp1910	2161597	2162877	p	-	unknown	conserved hypothetical protein	5.2
2029.2	4126	lpp1911	2163280	2164302	p	-	unknown		6
2849.1	4596	lpp1912	2165206	2165949	m	-	unknown		6
2848.4	4595	lpp1913	2166319	2166573	p	-	unknown		6
2847.4	4594	lpp1914	2166631	2167245	m	-	unknown		6
1283.2	3679	lpp1915	2167395	2168690	m	-	unknown	similar to unknown protein	5.2
1284.2	3680	lpp1916	2168677	2168958	m	-	unknown	similar to transcription regulators	3.5.2
1286.3	3681	lpp1917	2169198	2171090	m	-	unknown	similar to methyl transferase	4.6
1361.3	3721	lpp1918	2171105	2172148	m	-	unknown	Similar to conserved hypothetical protein	5.2
1360.6	3720	lpp1919	2172809	2174290	p	-	unknown	Similar to capsular polysaccharide biosynthesis protein	1.1
2841.4	4593	lpp1920	2174603	2175919	m	-	unknown	Similar to N-terminal part of polyketide synthase	4.6
2840.1	4592	lpp1921	2176089	2177612	m	-	unknown	similar to peptide antibiotic synthetase	4.6

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2838.1	4590	lpp1922	2177629	2178756	m	-	unknown	similar to acyl-coA dehydrogenase	2.4
2835.1	4589	lpp1923	2178826	2179680	m	+	unknown	similar to 3-hydroxybutyryl-CoA dehydrogenase	2.4
1693.2	3930	lpp1924	2179789	2180028	m	-	unknown	Similar to hypothetical protein	5.2
1695.2	3931	lpp1925	2180406	2181425	p	-	unknown	Similar to conserved hypothetical protein	5.2
2833.1	4588	lpp1926	2181607	2182590	m	+	unknown	similar to 3,5 -cyclic-nucleotide phosphodiesterase precursor (CpdP)	2.3
2831.1	4587	lpp1927	2182695	2183366	m	-	unknown	Similar to transcriptional regulator, LuxR family	3.5.2
2830.3	4586	lpp1928	2183632	2184222	m	-	unknown		6
5224.2	6045	lpp1929	2184210	2184572	m	-	unknown		6
3419.3	4929	lpp1930	2184863	2185621	p	-	unknown		6
3421.2	4931	lpp1931	2185721	2187055	m	-	unknown		6
3423.3	4932	lpp1932	2187286	2188482	p	-	RalF protein, translocated into host cells by the Dot/Icm system		
3426.1	4933	lpp1933	2188978	2189658	p	-	unknown	Weakly similar to sphingosine kinase	4.6
3428.1	4934	lpp1934	2189837	2190649	p	-	unknown	Similar to predicted phosphohydrolases	5.2
3429.1	4935	lpp1935	2190832	2193066	m	-	unknown		2.3
2250.2	4237	lpp1936	2193506	2194144	m	+	unknown		6
3431.4	4937	lpp1937	2194390	2195679	m	-	unknown	similar to other protein	6
3432.3	4938	lpp1938	2195679	2196782	m	-	unknown	similar to chloromuconate cycloisomerase	5.2
1889.2	4054	lpp1939	2197085	2198338	p	-	unknown		2.1.1
1887.2	4053	lpp1940	2198679	2200283	p	-	unknown	Some similarity with eukaryotic proteins	6
1704.4	3937	lpp1941	2200547	2202541	p	-	unknown		5.2
1703.1	3936	lpp1942	2202725	2203498	p	-	unknown		6
5724.2	6262	lpp1943	2203535	2205046	m	-	unknown		6
5723.2	6261	lpp1944	2205207	2205500	m	-	unknown	similar to unknown protein	5.2
6309.1	6364	lpp1945	2205526	2206611	m	-	Unknown	Similar to transposase (IS4 family)	4.5

Table XIV

4984.2	5936	lpp1946	2206829	2207395	p	-	unknown	similar to peptidyl-prolyl cis-trans isomerase proteins	3.9
5340.1	6091	lpp1947	2207576	2209132	m	-	unknown		6
5341.1	6092	lpp1948	2209468	2209695	m	-	unknown		6
5342.2	6093	lpp1949	2209957	2210517	p	-	unknown	Similar to transcriptional regulator, TetR family	3.5.2
5344.2	6094	lpp1950	2210666	2211325	p	-	unknown		6
6064.1	6328	lpp1951	2211382	2211624	m	+	unknown	hypothetical gene	6
4656.4	5729	lpp1952	2212041	2213834	m	-	unknown		6.
4657.1	5730	lpp1953	2214269	2214892	m	-	unknown	Similar to glutathione S-transferase	4.1
4658.2	5731	lpp1954	2214927	2215346	m	-	unknown	Similar to organic hydroperoxide resistance protein	4.2
4659.2	5732	lpp1955	2215573	2215950	m	-	unknown		6
4660.2	5733	lpp1956	2216182	2216343	p	-	unknown		6
4662.1	5734	lpp1957	2216796	2217038	p	-	unknown		5.1
4663.3	5735	lpp1958	2217507	2218400	p	+	major outer membrane protein		1.1
5901.3	6300	lpp1959	2218765	2220192	p	-	unknown	Some similarity with eukaryotic proteins. Pattern of chromosome condensation regulator conserved.	5.2
4566.1	5671	lpp1960	2220369	2220965	p	-	unknown	Similar to putative intracellular protease/amidase	2.2
4567.2	5672	lpp1961	2221035	2222930	m	-	unknown		6
5484.4	6153	lpp1962	2223205	2224569	p	+	unknown		6
1726.4	3952	lpp1963	2224659	2226323	p	-	unknown	Some similarity with eukaryotic proteins	5.2
4082.2	5347	lpp1964	2226507	2227706	p	-	unknown		6
806.2	6463	lpp1965	2227726	2228463	p	-	unknown	Similar to hydantoin-racemase	2.2
807.2	6464	lpp1966	2228503	2229816	m	-	unknown	Similar to guanine deaminase	2.3
808.4	6465	lpp1967	2229998	2232826	m	-	unknown		6
5602.3	6210	lpp1968	2233042	2233509	m	-	unknown	Similar to phosphohistidine phosphatase SixA	3.8
4365.4	5540	lpp1969	2233584	2234129	p	-	unknown	Similar to conserved hypothetical protein	5.2
4366.1	5541	lpp1970	2234228	2234644	p	-	unknown	putative membrane protein	6

Table XIV

4367.1	5542	lpp1971	2234931	2235569	m	-	unknown	Some similarity with eukaryotic proteins	5.2
4369.1	5543	lpp1972	2235773	2236423	m	-	unknown	predicted membrane protein	5.2
4370.1	5544	lpp1973	2236503	2237003	m	-	unknown		6
4371.1	5545	lpp1974	2237495	2238355	p	+	unknown	Similar to putative polysaccharide deacetylase-related protein	2.1.1
4372.3	5546	lpp1975	2238473	2239669	m	+	mltA	Similar to membrane-bound lytic murein transglycosylase	1.1
5270.2	6064	lpp1976	2239778	2240335	m	+	unknown		6
3133.2	4763	lpp1977	2240332	2241138	m	-	unknown		6
3132.1	4762	lpp1978	2241077	2241391	m	-	unknown		6
2146.2	4188	lpp1979	2241551	2242660	p	-	hisC	similar to histidinol-phosphate aminotransferase	2.2
2147.1	4189	lpp1980	2242697	2243038	p	-	unknown	similar to pterin-4- α -carbinolamine dehydratase phhB	2.5
2148.1	4190	lpp1981	2243216	2244133	m	-	secF	Similar to protein-export membrane protein SecF	1.6
949.3	6558	lpp1982	2244146	2246002	m	+	secD	Similar to protein-export membrane protein SecD	1.6
3131.1	4761	lpp1983	2246024	2246359	m	+	unknown	Similar to preprotein translocase	1.6
3130.1	4760	lpp1984	2246505	2247338	m	-	unknown		6
3129.2	4759	lpp1985	2247385	2248398	m	-	queA	adenosylmethionine:tRNA S-ribosyltransferase-isomerase	3.6
2509.3	4405	lpp1986	2248513	2248926	m	+	unknown	putative membrane protein	6
2510.2	4407	lpp1987	2249008	2250861	m	-	unknown	similar to ABC transporter ATP-binding protein	1.2
3128.1	4758	lpp1988	2250922	2251413	m	-	unknown	Similar to conserved hypothetical protein	5.2
468.3	5745	lpp1989	2251416	2251802	m	-	unknown	Similar to putative endoribonuclease L-PSP	3.6
469.3	5749	lpp1990	2251802	2253925	m	-	spot	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	2.3

Table XIV

470.3	5757	lpp1991	2254093	2254296	m	-	rpoZ	RNA polymerase omega subunit		3.5.3
472.1	5773	lpp1992	2254347	2254976	m	-	gmk	guanylate kinase	Similar to conserved hypothetical protein	2.3
473.2	5780	lpp1993	2254982	2255848	m	-		unknown		5.2
3127.1	4757	lpp1994	2256150	2256857	p	-	rph	Ribonuclease PH (RNase PH) (tRNA nucleotidyltransferase)		3.6
3124.2	4756	lpp1995	2257186	2258220	m	-		unknown	Similar to twitching motility protein PilT	1.5
3121.2	4755	lpp1996	2258384	2259076	p	-		unknown	Similar to conserved hypothetical protein	5.2
3119.1	4753	lpp1997	2259076	2259864	p	-	proC	unknown	similar to pyrroline-5-carboxylate reductase	2.2
5268.2	6063	lpp1998	2260208	2260783	p	-		unknown	Predicted integral membrane protein	5.2
574.2	6265	lpp1999	2260831	2261445	p	-		unknown		6
573.1	6263	lpp2000	2261459	2261740	p	-		unknown	Similar to conserved hypothetical protein	5.2
572.2	6260	lpp2001	2261894	2263582	m	+		unknown	Similar to serine protease	2.2
4457.2	5599	lpp2002	2263714	2264721	m	-		unknown	Similar to transcriptional regulator, AraC family	3.5.2
1626.3	3884	lpp2003	2264845	2266170	m	-	sahH	Adenosylhomocysteinase (S-adenosyl-L-homocysteinehydrolase)		2.2
1625.3	3883	lpp2004	2266189	2267337	m	-	metK	S-adenosylmethionine synthetase		2.2
865.2	6499	lpp2005	2267546	2268658	m	-	carA	carbamoyl-phosphate synthetase, glutamine (small subunit)		2.3
866.2	6500	lpp2006	2268754	2269893	m	-	dnaJ	chaperone protein DnaJ (heat shock protein)		4.1
3999.3	5287	lpp2007	2270082	2272016	m	-	dnak	Chaperone protein DnaK (Heat shock protein 70)		
3863.2	5209	lpp2008	2272161	2272760	m	-	grpE	(Heat shock 70 kDa protein) (HSP70) Heat-shock protein GrpE(HSP-70 cofactor)		4.1

Table XIV

3477.2	4963	lpp2029	2294190	2294927	m	-	unknown	Similar to ABC transporter ATP-binding protein	1.2
3476.1	4962	lpp2030	2294928	2296052	m	-	unknown	Similar to ABC transporter permease protein	1.2
3473.1	4961	lpp2031	2296146	2296997	p	-	unknown		6
3472.1	4960	lpp2032	2297124	2297423	p	+	unknown		6
1992.2	4110	lpp2033	2297567	2298625	m	-	unknown		6
707.2	6417	lpp2034	2298793	2299821	p	-	unknown	Similar to isopentenyl-diphosphate delta-isomerase	2.4
705.1	6416	lpp2035	2299812	2301110	p	-	unknown	Similar to 3-hydroxy-3-methylglutaryl-coenzyme A reductase	2.4
704.4	6415	lpp2036	2301107	2301985	p	-	unknown	Weakly similar to mevalonate kinase	5.2
5871.4	6288	lpp2037	2302584	2303759	m	-	Unknown	Similar to transposase (ISL3 family)	4.5
374.2	5138	lpp2038	2303825	2305591	m	-	unknown	Similar to poly(3-hydroxyalkanoate) synthetase	2.1.1
371.1	5123	lpp2039	2305902	2306213	p	-	unknown		6
1779.3	3985	lpp2040	2306423	2306608	m		Unknown	Similar to transposase (ISL3 family)	4.5
1780.3	3987	lpp2041	2306952	2307161	p	-	unknown	Similar to cold shock protein	4.1
1781.4	3988	lpp2042	2307401	2308807	p	-	unknown	Similar to ATP-dependent RNA helicase	3.6
1592.3	3865	lpp2043	2308964	2309875	p	+	unknown	Similar to cation efflux protein	1.2
4285.1	5484	lpp2044	2310147	2310548	m	+	unknown		6
4284.3	5483	lpp2045	2310564	2311646	m	-	unknown	similar to amidase	2.2
4282.3	5482	lpp2046	2311680	2312429	m	-	Unknown	Similar to transposase (IS5 family)	4.5
4281.2	5481	lpp2047	2312539	2312808	p	+	unknown		6
4276.2	5479	lpp2048	2313171	2315123	m	-	unknown		6
4532.2	5653	lpp2049	2315629	2317071	p	-	unknown		5.1
4531.2	5652	lpp2050	2317324	2317548	m	-	Unknown	Similar to transposase (IS5 family)	4.5
4530.1	5651	lpp2051	2317759	2318052	m	-	unknown	Similar to conserved hypothetical protein	5.2
4528.2	5649	lpp2052	2318078	2318863	m	-	Unknown	C-terminal part similar to transposase (IS4 family)	4.5
5504.4	6163	lpp2053	2319045	2319797	m	-	unknown		5.1

Table XIV

2357.4	4299	lpp2054	2320236	2322056	p	-	unknown	6	Similar to conserved hypothetical protein
864.1	6498	lpp2055	2322300	2322590	m	-	unknown	5.2	
863.1	6497	lpp2056	2322799	2323173	m	-	Unknown	4.5	Similar to transposase (IS5 family)
862.1	6496	lpp2057	2323533	2323784	p	-	Unknown	6.	
860.2	6495	lpp2058	2323929	2325671	p	-	unknown	5.2	Ankyrin repeat protein
3411.2	4922	lpp2059	2326169	2327248	p	-	unknown	6	
3413.2	4923	lpp2060	2327547	2328452	p	-	unknown	3.5.2	Similar to transcriptional regulator, LysR family
3414.3	4924	lpp2061	2328667	2330421	m	-	unknown	5.2	Ankyrin repeat protein
1910.6	4069	lpp2062	2330640	2335121	m	-	unknown	6	
1911.4	4070	lpp2063	2335445	2335906	m	-	unknown	4.6	putative cAMP/cGMP binding protein
1536.3	3828	lpp2064	2335956	2337833	m	+	unknown	1.2	Similar to potassium uptake protein
1603.3	3873	lpp2065	2338237	2339763	p	-	unknown	5.2	Putative ankyrin repeat protein
3878.1	5215	lpp2066	2339887	2342958	m	-	unknown	6	
3876.1	5214	lpp2067	2343282	2343770	p	+	unknown	5.2	Similar to conserved hypothetical proteins
3874.1	5213	lpp2068	2343839	2344093	m	-	unknown	6	
3872.1	5212	lpp2069	2344289	2344555	p	-	unknown	6	
3871.1	5211	lpp2070	2344580	2344969	p	-	unknown	6	Some similarities with eukaryotic proteins
5406.1	6119	lpp2071	2345221	2346759	m	-	Unknown	1.3	regulatory protein (GGDEF domain)
1307.4	3693	lpp2072	2346970	2348238	p	-	proline/glycine betaine transporter-like protein	1.2	
1306.5	3692	lpp2073	2348345	2351545	m	+	Chemiosmotic efflux system protein A-like protein	1.2	
5405.2	6118	lpp2074	2351546	2352514	m	+	Chemiosmotic efflux system protein B-like protein	1.2	
1001.3	3510	lpp2075	2352511	2353824	m	+	Chemiosmotic efflux system protein C-like protein	1.2	
1002.2	3511	lpp2076	2354183	2355811	m	-	unknown	3.8	Similar to protein kinase

Table XIV

4742.3	5789	lpp2077	2356163	2357077	p	-	unknown	Similar to transcriptional regulator, LysR family	3.5.2
4757.2	5799	lpp2078	2357089	2357676	m	-	unknown	similar to pyridoxamine 5-phosphate oxidase	2.5
4758.2	5800	lpp2079	2357810	2358190	m	-	unknown	similar to unknown proteins	5.2
4759.2	5801	lpp2080	2358285	2359049	p	-	unknown	Similar to 3-oxoacyl-[acyl-carrier protein] reductase	2.4
4760.2	5802	lpp2081	2359426	2360367	m	-	unknown		6
5065.2	5988	lpp2082	2360600	2361064	p	-	unknown	Protein with ankryrin repeat and a F-box domain	4.6
5066.2	5989	lpp2083	2361148	2361567	m	-	unknown	Similar to two-component response regulator	3.5.2
1643.4	3897	lpp2084	2361557	2364007	m	-	stuC		1.3
4500.1	5631	lpp2085	2364399	2364752	p	-	sensor histidine kinase		5.2
4498.1	5628	lpp2086	2365217	2366665	p	-	unknown	Similar to conserved hypothetical proteins	6
4497.4	5627	lpp2087	2366762	2368021	p	-	unknown		5.1
1937.4	4084	lpp2088	2368109	2368468	p	-	unknown		6
1939.5	4085	lpp2089	2368702	2369274	p	-	unknown		6
5542.3	6180	lpp2090	2369426	2370208	p	-	Unknown	Similar to aminoglycoside 6-adenylyltransferase	4.2
3904.3	5231	lpp2091	2370341	2372137	p	-	unknown	Similar to multidrug resistance ABC transporter ATP-binding protein	1.2
440.4	5569	lpp2092	2372425	2377026	p	-	SdeC protein, substrate of the Dot/Icm system		5.1
3908.3	5232	lpp2093	2377240	2378361	p	-	unknown	similar to L. pneumophila SdeA protein	5.1
3714.3	5127	lpp2094	2378414	2381038	p	-	unknown		6
817.7	6468	lpp2095	2381318	2387080	p	-	substrates of the Legionella pneumophila Dot/Icm system		5.1
1933.4	4081	lpp2096	2387451	2392088	p	-	SdeB		5.1
3003.1	4688	lpp2097	2392571	2393194	p	-	sdeA		5.1
3002.1	4687	lpp2098	2393223	2394344	m	-	unknown	Similar to methyltransferase similar to (hydroxyindole) O-methyltransferase	2.1.1
2436.2	4355	lpp2099	2394630	2395997	m	-	unknown		2.2
3000.1	4686	lpp2100	2396605	2398863	p	-	unknown	similar to conserved hypothetical protein	5.1
						-			5.2

Table XIV

1444.3	3772	lpp2128	2421091	2422908	m	-	unknown	Similar to eukaryotic sphingosine-1-phosphate lyase 1	2.4
1870.3	4042	lpp2129	2423146	2424252	p	+	unknown	Similar to multidrug efflux RND membrane fusion protein MexE	1.2
630.4	6363	lpp2130	2424352	2427504	p	-	unknown	Similar to RND multidrug efflux transporter	1.2
3205.3	4802	lpp2131	2427666	2431985	p	-	unknown	similar to peptide synthase	4.6
3207.5	4803	lpp2132	2432106	2434589	p	-	unknown	Similar to two component sensor histidine kinase	1.3
4830.2	5850	lpp2133	2434761	2435669	p	-	unknown	Similar to response regulator	3.5.2
4833.2	5851	lpp2134	2435951	2436712	p	-	unknown	Similar to eukaryotic SAM dependent methyltransferase	4.6
5247.1	6055	lpp2135	2436737	2437771	p	-	unknown	Similar to conserved hypothetical protein	5.2
1205.5	3632	lpp2136	2438029	2449374	p	-	unknown	similar to polyketide synthase of type I	4.6
1207.2	3633	lpp2137	2449377	2449778	m	+	unknown		6
2949.2	4641	lpp2138	2450005	2450958	m	-	unknown	Similar to putative transport proteins	1.2
2951.2	4643	lpp2139	2451420	2453423	p	-	unknown	Some similarity with eukaryotic proteins	6
2952.1	4644	lpp2140	2453536	2455377	m	-	unknown	Present a domain similar to Icml protein	5.2
2953.2	4645	lpp2141	2455913	2456413	p	-	gspA global stress protein GspA		4.1
2204.2	4216	lpp2142	2456595	2458115	p	+	unknown	Similar to sulfate transporters	1.2
2207.2	4217	lpp2143	2458119	2458745	p	-	unknown	Similar to carbonic anhydrase proteins	4.7
2208.1	4218	lpp2144	2458863	2459156	m	-	unknown	hypothetical gene	6
2209.4	4219	lpp2145	2459187	2460158	m	-	unknown	similar to ornithine cyclodeaminase	2.2
2557.4	4433	lpp2146	2460213	2460659	m	-	unknown	Similar to ketosteroid isomerase homolog	2.4
2555.5	4432	lpp2147	2461033	2462187	p	-	unknown		6
4613.3	5701	lpp2148	2462381	2463862	p	+	unknown	Similar to transporters	1.2
4609.2	5700	lpp2149	2463867	2464448	m	-	unknown		6
4608.1	5699	lpp2150	2464665	2465201	m	-	unknown		6
4607.3	5698	lpp2151	2465334	2466764	m	-	unknown	similar to unknown proteins	5.2

Table XIV

5610.1	6216	lpp2152	2466798	2467241	m	-	unknown	similar to unknown protein	5.2
5609.1	6214	lpp2153	2467211	2467495	m	-	unknown	Similar to conserved hypothetical protein	5.2
5084.4	5998	lpp2154	2467579	2469132	m	-	unknown	Periplasmic protein weakly similar to AlgJ	5.2
5607.2	6213	lpp2155	2469135	2470556	m	-	unknown	Similar to alginate o-acetyltransferase AlgI	2.1.1
5606.2	6212	lpp2156	2470772	2471410	p	-	unknown	Predicted integral membrane protein	6
1317.3	3696	lpp2157	2471646	2472746	p	+	unknown		6
1318.5	3697	lpp2158	2472794	2474017	m	-	unknown	similar to unknown protein	5.2
4547.4	5662	lpp2159	2474360	2475373	m	-	unknown	Similar to oxidoreductase	2.1.1
4171.4	5414	lpp2160	2475691	2476218	p	+	unknown	similar to conserved hypothetical protein	5.2
4172.2	5415	lpp2161	2476367	2477428	m	-	unknown		6
4173.2	5416	lpp2162	2477564	2477968	m	-	unknown	similar to conserved hypothetical protein	5.2
2526.3	4417	lpp2163	2478168	2479442	p	-	unknown		6
4174.1	5417	lpp2164	2479719	2480135	p	+	unknown	Similar to hemin binding protein Hbp	5.1
4175.1	5418	lpp2165	2480232	2481155	m	-	unknown	Similar to hypothetical sugar nucleotide epimerase	2.1.1
4177.2	5419	lpp2166	2481235	2482830	m	-	unknown		6
5557.2	6189	lpp2167	2482851	2484623	m	-	unknown	Some similarity with eukaryotic protein	5.2
4636.4	5715	lpp2168	2485250	2489992	p	-	unknown	Some similarity with eukaryotic protein	5.2
1903.4	4064	lpp2169	2490228	2491202	m	-	unknown	similar to chitinase	2.1.1
5796.5	6272	lpp2170	2491410	2492495	p	-	unknown	Similar to choline monoxygenase	2.1.1
549.6	6155	lpp2171	2492656	2493777	p	-	unknown	similar to unknown proteins	5.2
548.3	6150	lpp2172	2493840	2495339	m	+	unknown		6
3306.4	4866	lpp2173	2495482	2496201	m	+	unknown		6
3304.2	4865	lpp2174	2496579	2497700	m	+	Unknown	similar to unknown protein	5.2
3303.3	4864	lpp2175	2497962	2499185	m	-	unknown		6
1088.4	3562	lpp2176	2499394	2500923	m	-	unknown	similar to other proteins	5.2
1087.2	3561	lpp2177	2500930	2502621	m	-	unknown	similar to acyl-CoA dehydrogenase	2.4

Table XIV

3301.2	4863	lpp2178	2502630	2504051	m	-	unknown	similar to propionyl-CoA carboxylase beta chain	2.4
3299.4	4860	lpp2179	2504273	2505046	m	-	unknown	similar to outer membrane protein	1.1
3297.3	4859	lpp2180	2505791	2506852	p	-	unknown	Similar to 3-oxoacyl-[acyl-carrier-protein] synthase III	2.4
1412.5	3754	lpp2181	2506864	2508609	p	-	unknown	Similar to acyl-CoA synthetase	2.4
1413.2	3755	lpp2182	2508614	2509993	p	-	unknown	Similar to acyl-CoA synthetase	2.4
1414.1	3756	lpp2183	2509983	2510216	p	-	unknown	similar to acyl carrier protein (ACP)	2.4
1415.4	3757	lpp2184	2510213	2510965	p	-	unknown	Similar to 3-oxoacyl-[acyl-carrier-protein] reductase	2.4
2900.2	4613	lpp2185	2510962	2511972	p	-	unknown	Similar to 3-oxoacyl-(acyl-carrier-protein) synthase III	2.4
2898.4	4610	lpp2186	2512292	2512519	m	-	unknown	Similar to acyl-carrier protein	2.4
1840.3	4024	lpp2187	2512529	2513752	m	-	unknown	Similar to multidrug resistance protein	1.2
1839.2	4022	lpp2188	2513906	2515108	p	-	unknown	similar to sterol desaturase-related protein	2.4
2893.2	4609	lpp2189	2515261	2517603	p	-	unknown	similar to nitric oxide reductase	4.2
2891.2	4608	lpp2190	2517794	2519626	m	-	unknown	similar to multidrug resistance ABC transporter ATP-binding protein	1.2
2889.2	4607	lpp2191	2519788	2520174	m	+	unknown	Putative membrane protein	5.2
2544.3	4425	lpp2192	2520386	2524243	p	-	unknown		6
2268.2	4246	lpp2193	2524479	2525687	p	-	unknown	Similar to conserved hypothetical protein	5.2
2266.2	4245	lpp2194	2525774	2527042	p	-	unknown	Similar to GTP cyclohydrolase II	2.5
2264.2	4244	lpp2195	2526993	2528276	p	-	unknown	similar to hypothetical protein	5.2
1239.2	3651	lpp2197	2528262	2529245	p	-	Unknown		6.
1242.2	3653	lpp2196	2528289	2528933	p	-	unknown	Similar to uracil phosphoribosyltransferase (upp)	2.3
1238.2	3650	lpp2198	2529239	2532139	p	-	unknown		6
5188.2	6030	lpp2199	2532404	2533696	m	-	unknown	Similar to C4-dicarboxylate transport protein	1.2
5189.2	6031	lpp2200	2534017	2534526	m	+	unknown		6
3235.4	4819	lpp2201	2535075	2535731	p	-	unknown	Similar to hypothetical protein DedA	5.2

Table XIV

3236.3	4820	lpp2202	2535795	2538029	m	-	unknown	6	
926.4	6542	lpp2203	2538120	2538818	m	-	unknown	2.2	Similar to amidotransferase
928.1	6543	lpp2204	2538948	2540108	m	-	unknown	2.1.1	similar to alcohol dehydrogenase
929.2	6544	lpp2205	2540238	2541635	m	-	unknown	2.1.1	similar to aldehyde dehydrogenase
1788.3	3993	lpp2206	2541673	2543046	m	-	unknown	2.2	Similar to glutamine synthase
1792.2	3995	lpp2207	2543098	2543886	m	-	unknown	5.2	Similar to hypothetical protein
3238.1	4821	lpp2208	2543883	2544746	m	-	unknown	5.2	similar to conserved hypothetical protein
1116.2	3583	lpp2209	2544822	2545073	m	+	unknown	6	
1118.2	3584	lpp2210	2545503	2546861	m	-	unknown	4.2	Similar to metallo-beta-lactamase superfamily proteins
1119.2	3585	lpp2211	2546984	2547634	m	-	unknown	6	
3239.1	4822	lpp2212	2547751	2548041	p	+	unknown	6	Putative membrane protein
3240.3	4824	lpp2213	2548132	2548443	m	-	unknown	6	
4192.2	5428	lpp2214	2548660	2550447	p	-	unknown	2.1.1	Similar to poly(3-hydroxyalkanoate) synthetase
4191.1	5427	lpp2215	2550459	2551865	p	-	unknown	2.1.1	similar to phosphotransacetylase
4188.1	5425	lpp2216	2551862	2552980	p	-	acetate kinase	2.1.2	
4186.1	5424	lpp2217	2553019	2553909	p	-	unknown	4.1	Similar to curved DNA-binding protein (sequence similarity to chaperone protein dnaJ)
4184.1	5423	lpp2218	2553912	2554226	p	-	unknown	5.2	similar to unknown protein
1647.2	3900	lpp2219	2554223	2554786	m	-	unknown	2.1.1	Similar to acyltransferase
1645.1	3899	lpp2220	2554904	2555455	p	-	unknown	5.2	Similar to conserved hypothetical protein
1644.6	3898	lpp2221	2555488	2556726	m	-	unknown		Similar to imidazolonepropionase and related amidohydrolases
2583.3	4447	lpp2222	2556927	2557487	p	-	unknown	2.2	
2582.3	4446	lpp2223	2557435	2560011	p	-	unknown	6	Putative membrane protein
4809.2	5836	lpp2224	2560039	2560881	p	-	unknown	5.2	Similar to conserved hypothetical protein
4810.1	5838	lpp2225	2561033	2561683	p	-	unknown	5.2	Similar to conserved hypothetical protein
4811.2	5839	lpp2226	2561857	2562345	m	+	unknown	6	
								5.2	Putative membrane protein

Table XIV

1768.3	3978	lpp2227	2562490	2563803	m	-	ugpB	unknown	Similar to glycerol-3-phosphate-binding periplasmic protein precursor	1.2
1767.2	3977	lpp2228	2563800	2564519	m	-		unknown	Similar to glycerophosphodiester phosphodiesterase	2.4
4826.2	5849	lpp2229	2564524	2565219	m	+		unknown	Similar to hypothetical protein	5.2
4073.1	5341	lpp2230	2565909	2566982	p	-		unknown	Similar to leucine dehydrogenase	2.2
4072.1	5340	lpp2231	2566997	2567653	p	-		unknown	Similar to O-methyltransferase	2.1.1
997.2	6588	lpp2232	2567720	2568766	p	-	lly	4-hydroxyphenylpyruvate dioxygenase (legiolysin)		
996.2	6587	lpp2233	2568822	2569820	p	-		unknown	similar to unknown protein	2.1.1 5.2
995.2	6586	lpp2234	2569817	2570455	p	-		unknown	Similar to glutathione S-transferase (maleylacetate isomerase)	4.1 6
4071.1	5339	lpp2235	2570452	2571012	m	-		unknown		
4070.3	5338	lpp2236	2571160	2572563	p	-	asnS	asparagine tRNA synthetase		3.7.2 6
4678.3	5744	lpp2237	2572560	2572958	m	-		unknown	similar to ATP-binding component of ABC transporter	1.2
4680.2	5746	lpp2238	2572982	2573665	m	-		unknown	Similar to ABC transporter permease component	1.2
4683.3	5747	lpp2239	2573658	2574905	m	+		unknown	Similar to CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	2.4 2.6
5492.2	6156	lpp2240	2575722	2576285	m	+	pgsA	unknown	Similar to phosphatase	3.6 6 3.6
4356.2	5536	lpp2241	2576306	2576965	m	-		unknown		
4355.3	5535	lpp2242	2576958	2577905	m	-	rluC	Ribosomal large subunit pseudouridine synthase		
4354.3	5534	lpp2243	2578258	2578455	p	-		unknown		
787.3	6455	lpp2244	2578804	2580795	p	-	rne	Ribonuclease E		
789.4	6456	lpp2245b	2581017	2581268	m	-		Unknown	Similar to transposase (IS4 family)	4.5
6165.1	6342	lpp2245a	2581389	2582213	m	-		Unknown	Similar to transposase (IS4 family)	4.5 6
1159.5	3608	lpp2246	2582461	2583738	m	-		unknown		

Table XIV

1681.5	3921	lpp2247	2584331	2587207	p	-	hepA	RNA polymerase-associated protein HepA	similar to ankyrin repeat domain protein	3.5.3
248.2	4386	lpp2248	2587321	2588724	m	-		unknown		5.2
247.1	4379	lpp2249	2588725	2589498	m	-		unknown		6
245.1	4365	lpp2250	2589646	2590668	m	-	asd	Aspartate-semialdehyde dehydrogenase		2.2
244.1	4358	lpp2251	2590778	2591836	m	-	aroC	chorismate synthase		2.2
243.2	4351	lpp2252	2591848	2592780	m	-		unknown	similar to putative adenine-specific methylase	3.2
2017.1	4118	lpp2253	2592945	2593514	p	-		unknown	similar to conserved hypothetical protein	5.2
2016.2	4117	lpp2254	2593587	2594006	p	-		unknown	similar to conserved hypothetical protein	5.2
3028.1	4703	lpp2255	2594011	2594265	p	-	grx	unknown	Similar to glutaredoxin Grx	4.6
3027.1	4702	lpp2256	2594275	2594763	p	-	secB	unknown	similar to protein-export protein SecB	1.6
376.3	5150	lpp2257	2594765	2595754	p	+	gpsA	unknown	similar to glycerol-3-phosphate dehydrogenase (NAD+)	2.1.1
377.1	5155	lpp2258	2595832	2596671	m	-	murI	unknown	similar to glutamate racemase	2.2
381.6	5177	lpp2259	2596741	2600256	m	-		unknown		6
5899.1	6297	lpp2260	2600402	2600704	p	+		unknown		6
1823.5	4015	lpp2261	2600708	2602000	m	-		unknown	Similar to conserved hypothetical protein	5.2
4346.2	5528	lpp2262	2602255	2603127	m	-	dapA	dihydrodipicolinate synthase		2.2
4347.2	5529	lpp2263	2603339	2603593	p	+		unknown		6
4349.2	5530	lpp2264	2603871	2604653	p	+		unknown	Similar to 3-hydroxybutyrate dehydrogenase	2.4
4350.2	5531	lpp2265	2604660	2605820	p	-		unknown	Similar to conserved hypothetical protein	5.2
4351.2	5532	lpp2266	2605850	2606755	p	-	motA2	unknown	similar to proton conductor component of motor, chemotaxis and motility protein	1.5
4352.3	5533	lpp2267	2606765	2607703	p	-	motB2	unknown	similar to flagellar motor protein	1.5
5986.2	6314	lpp2268	2607769	2608242	m	-		unknown		6
4691.2	5751	lpp2269	2608487	2609782	p	-	sdaC	unknown	Similar to serine transporter	1.2
4690.2	5750	lpp2270	2609875	2611800	m	-		unknown	ankyrin repeat protein	6

Table XIV

4688.2	5748	lpp2271	2611887	2613008	m	-	unknown	similar to type II secretion system protein-like protein and twitching motility protein	1.6 6
405.3	5323	lpp2272	2613098	2615026	m	-	unknown		
406.1	5330	lpp2273	2615313	2616149	m	-	unknown	Similar to hypothetical protein	5.2
407.4	5337	lpp2274	2616146	2617498	m	-	radA	Similar to DNA repair protein RadA	3.2 6
5420.2	6123	lpp2275	2617733	2618611	p	-	unknown		
5422.1	6124	lpp2276	2618876	2619259	p	-	unknown	Unknown, N-terminal similar to Legionella 33 kDa polypeptide	5.1
5423.1	6125	lpp2277	2619453	2619683	p	-	xseB	Similar to exodeoxyribonuclease VII, small subunit	2.3
2225.2	4226	lpp2278	2619664	2620560	p	-	unknown	Similar to geranyltranstransferase; farnesyl-diphosphate synthase	2.4
1128.3	3592	lpp2279	2620604	2621458	m	-	unknown	Similar to biotin synthesis protein	2.5
1132.2	3593	lpp2280	2621502	2622206	p	-	unknown	Similar to competence protein ComF	1.2
1133.3	3594	lpp2281	2622235	2623302	m	-	unknown	Similar to membrane-associated metalloprotease proteins	2.2 6
1134.3	3595	lpp2282	2623365	2623643	m	-	unknown		
3802.2	5173	lpp2283	2623961	2625235	p	-	hemA	glutamyl tRNA reductase	2.5
3803.1	5174	lpp2284	2625219	2626307	p	-	prfA	peptide chain release factor 1	3.7.5
3804.2	5175	lpp2285	2626300	2627163	p	-	hemK	Similar to methyltransferase hemK	3.8
3807.2	5176	lpp2286	2627307	2627738	p	-	dksA	Similar to DnaK suppressor protein	4.1 6
1407.2	3750	lpp2287	2627808	2628641	p	-	unknown		
1406.2	3749	lpp2288	2628646	2629905	m	-	kdtA	3-Deoxy-D-manno-oct-2-ulosonic acid transferase	1.1 3.9 6
1405.2	3748	lpp2289	2630060	2630950	p	-	djIA	Similar to DnaJ-like protein	2.4 6
5424.2	6126	lpp2290	2630917	2631690	m	+	unknown		
5134.4	6019	lpp2291	2631882	2632811	m	+	plaA	lysophospholipase A	
5133.3	6018	lpp2292	2633081	2633596	p	-	unknown		

Table XIV

5132.3	6017	lpp2293	2633753	2633971	m	-	unknown	6	Similar to ATP-dependent RNA helicase dead (cold-shock DEAD-box protein A)
3072.2	4724	lpp2294	2634322	2636091	m	-	dead	3.6	Similar to conserved hypothetical protein
640.2	6377	lpp2295	2636459	2637376	m	-	unknown	5.2	Similar to 2,4-dienoyl-CoA reductase
641.3	6379	lpp2296	2637373	2639397	m	-	fadH	2.4	Similar to alkyl hydroperoxide reductase AhpD
1618.3	3880	lpp2297	2639702	2640190	p	+	sodC	4.2	Similar to alkyl hydroperoxide reductase AhpC
1617.3	3879	lpp2298	2640234	2640749	m	-	unknown	6	Similar to MutT/nudix family protein
2152.2	4195	lpp2299	2640772	2641311	m	-	unknown	2.1.3	Similar to oxygen-independent coproporphyrinogen III oxidase
3074.1	4725	lpp2300	2641511	2642362	p	-	unknown	2.3	Similar to amidase
1880.3	4048	lpp2301	2642460	2643452	m	-	mdh	2.2	Predicted membrane protein
2459.1	4371	lpp2302	2643442	2644002	m	-	unknown	5.2	Similar to O-sialoglycoprotein endopeptidase
2458.2	4370	lpp2303	2644084	2645211	p	-	hemN	2.2	Similar to conserved hypothetical protein
2162.2	4201	lpp2304	2645243	2646652	m	-	unknown	3.7.1	Similar to transposase
2164.2	4202	lpp2305	2647006	2647839	p	-	unknown	4.5	Similar to integrase
1902.5	4063	lpp2306	2648138	2649139	m	-	gcp	4.4	Similar to L.pneumophila proline/betaine transport protein homolog CitA (TphA)
5369.2	6100	lpp2307	2649344	2649583	p	-	rpsU	6	Similar to acetyltransferase
5370.1	6102	lpp2308	2649786	2650229	p	-	lporfX	2.1.1	Similar to hydrolase
2282.4	4254	lpp2309	2650238	2651971	p	-	dnaG		
1169.3	3614	lpp2310	2652058	2653923	p	-	rpoD		
5920.3	6306	lpp2311	2654264	2655439	m	-	unknown		
879.3	6507	lpp2312	2655505	2656599	m	-	unknown		
876.1	6506	lpp2313	2657086	2657556	m	-	unknown		
875.5	6505	lpp2314	2657573	2658847	m	+	unknown		
5474.2	6145	lpp2315	2658825	2659337	m	-	unknown		
3234.3	4818	lpp2316	2659379	2660062	p	-	unknown		

Table XIV

3233.1	4817	lpp2317	2660089	2660892	p	-	unknown	Putative transcriptional regulator	3.5.2
3232.1	4816	lpp2318	2660976	2661215	p	-	Unknown		6.
3231.1	4815	lpp2319	2661440	2661604	p	-	unknown		6
3230.1	4814	lpp2320	2661761	2662192	p	+	unknown		6
3228.1	4812	lpp2321	2662287	2662496	p	-	unknown	Similar to cold shock protein	4.1
151.2	3810	lpp2322	2662582	2663325	p	-	unknown	Similar to acetoacetyl-CoA reductase	2.4
150.3	3804	lpp2323	2663613	2665427	m	-	unknown	similar to polyhydroxyalkanoic-acid-synthase	2.1.1
148.2	3792	lpp2324	2665695	2667215	m	-	Unknown	regulatory protein (GGDEF and EAL domains)	1.3
2024.2	4123	lpp2325	2667181	2667723	m	-	unknown	Similar to conserved hypothetical protein	5.2
3226.2	4811	lpp2326	2668073	2668336	p	-	unknown	Similar to transcriptional regulator, SinR family	3.5.2
2639.1	4475	lpp2327	2669395	2669844	p	+	unknown		6
1423.2	3763	lpp2328	2670182	2671606	p	-	unknown	similar to ATP synthase beta chain	1.4
1424.2	3764	lpp2329	2671615	2672025	p	-	unknown	Similar to ATP synthase epsilon chain (atpC)	1.4
1425.2	3765	lpp2330	2672015	2672293	p	-	unknown	similar to putative ATP synthase subunit	1.4
1548.2	3834	lpp2331	2672296	2672988	p	-	unknown	similar to ATP synthase A chain	1.4
1549.1	3835	lpp2332	2672985	2673260	p	+	unknown	similar to ATP synthase C chain	1.4
1550.2	3836	lpp2333	2673266	2674009	p	-	unknown	Similar to ATP synthase B chain	1.4
819.2	6470	lpp2334	2673996	2675468	p	-	unknown	Similar to ATP synthase alpha chain	1.4
818.2	6469	lpp2335	2675526	2676395	p	-	unknown	Similar to ATP synthase gamma chain	1.4
2637.1	4474	lpp2336	2676427	2676801	m	-	unknown		6
1631.3	3888	lpp2337	2677149	2679032	p	-	unknown	Similar to NADH oxidoreductase	1.4
1629.1	3886	lpp2338	2679032	2679793	p	+	unknown	similar to unknown protein	5.2
1628.3	3885	lpp2339	2679790	2680608	p	+	unknown	similar to putative cytochrome c family protein.	1.4
1960.2	4096	lpp2340	2680674	2681174	m	+	unknown	predicted membrane protein	6
158.2	3854	lpp2341	2681171	2681836	m	-	unknown	Predicted membrane protein, similar to hypothetical protein	5.2

Table XIV

159.1	3862	lpp2342	2681842	2682135	m	-	unknown	similar to unknown protein	5.2
160.1	3870	lpp2343	2682331	2682654	p	+	unknown		6
163.1	3887	lpp2344	2682882	2684180	m	-	gdhA unknown	Similar to glutamate dehydrogenase	2.2
166.2	3909	lpp2345	2684358	2687552	m	-	copA2 unknown	Similar to copper efflux ATPase	1.2
168.1	3920	lpp2346	2687471	2687998	m	-	unknown	predicted transmembrane protein	5.2
169.1	3927	lpp2347	2688144	2688350	p	-	unknown		5.1
592.3	6305	lpp2348	2688363	2690042	m	-	unknown		5.1
593.2	6308	lpp2349	2690279	2690590	p	-	unknown		6
594.1	6309	lpp2350	2690729	2691181	m	+	cecA Chemiosmotic efflux system C protein A		1.2
157.2	3849	lpp2351	2691178	2694393	m	+	cecA Chemiosmotic efflux system protein A-like protein		1.2
154.1	3830	lpp2352	2694394	2695362	m	+	cecB Chemiosmotic efflux system C protein B		1.2
153.2	3823	lpp2353	2695359	2696672	m	+	cecC Chemiosmotic efflux system C protein C		1.2
152.3	3818	lpp2354	2696697	2697056	m	+	unknown	Similar to outer membrane lipoprotein	1.1
1961.3	4097	lpp2355	2697208	2698089	m	-	Unknown	regulatory protein (GGDEF domain)	1.3
234.2	4286	lpp2356	2698228	2700438	m	-	copA1 unknown	similar to copper efflux ATPase	1.2
228.1	4253	lpp2357	2700502	2700669	m	-	unknown		6
227.2	4247	lpp2358	2700694	2701605	m	-	unknown	Similar to ribose-phosphate pyrophosphokinase	2.3
111.2	3580	lpp2359	2701602	2703155	m	-	unknown	similar to thymidine/pyrimidine- nucleoside phosphorylase	2.3
109.1	3564	lpp2360	2703113	2704525	m	-	unknown	Similar to metallo-beta-lactamase superfamily proteins	4.2
107.1	3553	lpp2361	2704471	2707614	m	-	cebA Chemiosmotic efflux system B protein A		1.2
104.1	3533	lpp2362	2707689	2708822	m	+	cebB Chemiosmotic efflux system B protein B		1.2
103.1	3525	lpp2363	2708819	2710078	m	+	cebC Chemiosmotic efflux system B protein C		1.2
102.1	3519	lpp2364	2710065	2712755	m	-	ctpA unknown	similar to cation transport ATPase	1.2

Table XIV

99.1	6582	lpp2365	2712946	2713077	p	-	unknown	hypothetical gene	6
97.2	6568	lpp2366	2713176	2713448	p	-	unknown	hypothetical gene	6
96.6	6562	lpp2367	2713576	2714433	p	-	unknown		5.1
743.4	6432	lpp2368	2715263	2715658	p	-	unknown		5.2
744.4	6433	lpp2369	2715673	2716179	m	-	cadA1	similar to cadmium-transporting ATPase (C-terminal part)	4.2
747.4	6434	lpp2370	2717023	2719158	m	-	cadA2	similar to cation transport ATPase	1.2
2631.5	4473	lpp2371	2719234	2722383	m	-	helA	HelA protein	1.2
2627.1	4471	lpp2372	2722393	2723649	m	+	helB	HelB protein	1.2
1804.2	4004	lpp2373	2723646	2724890	m	+	helC	HelC protein	1.2
1803.2	4003	lpp2374	2725059	2725175	m	-		unknown	5.2
2626.1	4470	lpp2375	2725344	2726006	m	-		unknown	4.4
2625.2	4469	lpp2376	2726191	2727063	p	-		unknown	5.1
5812.1	6278	lpp2377	2726921	2727391	p	-		unknown	5.1
5813.1	6279	lpp2378	2727411	2727608	p	-		unknown	5.1
5814.1	6280	lpp2379	2727605	2728039	p	+		Unknown	6
4109.2	5365	lpp2380	2728036	2728626	p	+		unknown	5.2
4108.1	5364	lpp2381	2728637	2729473	p	+		unknown	5.2
1376.2	3729	lpp2382	2729475	2729933	p	-		unknown	5.2
1375.2	3728	lpp2383	2729924	2730622	p	+		unknown	5.2
1373.1	3727	lpp2384	2730632	2730958	p	-		unknown	6
1372.2	3726	lpp2385	2730961	2731224	p	-		unknown	6
2367.2	4306	lpp2386	2731227	2731613	p	+		unknown	6
4107.1	5363	lpp2387	2731622	2731972	p	-		unknown	6
4106.1	5362	lpp2388	2731977	2732639	p	+		unknown	5.2
4105.1	5361	lpp2389	2732626	2733408	p	+		unknown	
4104.2	5360	lpp2390	2733405	2734718	p	-		unknown	5.2
								putative secreted protein	5.2
								Similar to conserved hypothetical protein, putative secreted protein	5.2
								Similar to conserved hypothetical protein	5.2

Table XIV

5517.1	6167	lpp2391	2734675	2735064	p	+	unknown	Similar to conserved hypothetical protein, putative secreted protein	5.2
1287.3	3682	lpp2392	2735075	2737849	p	-	unknown	Similar to type IV secretory pathway, VirB4 components	1.6
4822.3	5848	lpp2393	2737758	2738819	p	-	unknown	Similar to conserved hypothetical protein	5.2
1623.4	3881	lpp2394	2738829	2740211	p	-	unknown	Similar to conserved hypothetical protein	5.2
1624.5	3882	lpp2395	2740213	2741781	p	-	unknown	Similar to conserved hypothetical protein	5.2
4233.4	5452	lpp2396	2741784	2741993	m	+	unknown		6
4234.4	5453	lpp2397	2742007	2742339	p	+	unknown	hypothetical gene	6
4236.4	5454	lpp2398	2742343	2744349	p	-	unknown	Similar to conserved hypothetical protein	5.2
4238.1	5455	lpp2399	2744351	2744833	p	-	unknown		6
4239.4	5456	lpp2400	2744922	2745209	m	-	unknown	hypothetical gene	6
5576.3	6197	lpp2401	2745277	2746245	m	-	Unknown		6.
6160.1	6341	lpp2402	2746636	2747811	m	-	Unknown	Similar to transposase (ISL3 family)	4.5
5987.2	6315	lpp2403	2748197	2749000	p	-	unknown		6
5626.3	6221	lpp2404	2748993	2749895	p	-	unknown	Weakly similar to integrase	4.5
1920.3	4074	lpp2405	2750070	2751128	p	+	unknown	Similar to cobalt-nickel resistance system protein	1.2
1923.2	4075	lpp2406	2751783	2751974	p	-	unknown		6
1924.4	4076	lpp2407	2752031	2752537	p	-	unknown	Similar to antirestriction protein	3.2
3258.2	4836	lpp2408	2752559	2753485	m	-	unknown	Similar to conserved hypothetical protein	5.2
3257.2	4835	lpp2409	2753475	2753927	m	-	unknown	Similar to hypothetical protein	5.2
6159.1	6339	lpp2410	2754296	2755276	m	-	Unknown	Similar to transposase (ISL3 family)	4.5
5890.1	6292	lpp2411	2755537	2755635	m	-	Unknown	Similar to transposase (ISL3 family) - partial	4.5
3653.3	5083	lpp2412	2755742	2755915	m	-	unknown		6
3655.1	5084	lpp2413	2756221	2756919	m	-	unknown	weakly similar to serine/threonine protein kinase	3.8
510.2	6008	lpp2414	2756912	2757601	m	-	unknown		6
509.1	6001	lpp2415	2757715	2758308	m		unknown	similar to unknown proteins	5.2
507.3	5992	lpp2416	2758338	2758478	m	-	Unknown	Similar to transposase - partial	4.5

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506.3	5983	lpp2417	2759103	2759459	p	-	unknown	6
505.3	5976	lpp2418	2759500	2760432	m	-	unknown	6
3657.1	5085	lpp2419	2760752	2761390	m	-	unknown	6.
3658.1	5086	lpp2420	2761865	2762041	p	-	unknown	6
948.3	6557	lpp2421	2762052	2762537	p	-	unknown	4.5
947.3	6556	lpp2422	2762506	2762868	m	-	unknown	5.2
946.3	6555	lpp2423	2762906	2763514	m	-	unknown	5.2
3659.2	5087	lpp2424	2763698	2764150	m	-	unknown	6.
3661.4	5089	lpp2425	2764204	2765190	m	+	unknown	5.2
5620.3	6218	lpp2426	2765844	2766071	p	-	unknown	3.5.2
2153.3	4196	lpp2427	2766068	2766304	p	-	unknown	6
426.3	5470	lpp2428	2766613	2767311	p	-	unknown	6
6369.1	6373	lpp2429	2767308	2767526	p	-	unknown	4.5
425.1	5465	lpp2430	2767602	2767829	m	-	unknown	6
424.1	5457	lpp2431	2767876	2768187	m	-	unknown	5.2
423.2	5449	lpp2432	2768203	2769495	m	+	unknown	5.2
5621.1	6219	lpp2433	2769530	2770738	m	+	unknown	1.2
5623.2	6220	lpp2434	2771034	2772428	m	-	unknown	6
3891.2	5222	lpp2435	2772433	2773068	m	-	unknown	5.2
3890.2	5221	lpp2436	2773237	2774583	p	-	unknown	6
3889.1	5219	lpp2437	2774573	2775328	m	-	unknown	5.2
3888.1	5218	lpp2438	2775331	2775528	m	-	unknown	6
3887.1	5217	lpp2439	2775548	2776774	m	-	unknown	1.2
3884.2	5216	lpp2440	2777410	2777883	p	-	unknown	6
1432.3	3767	lpp2441	2778073	2778990	p	-	unknown	3.5.2
1429.4	3766	lpp2442	2779173	2780660	m	+	unknown	6
5404.2	6117	lpp2443	2781074	2781973	m	-	unknown	6
5402.1	6116	lpp2444	2782135	2783574	p	-	unknown	6
2533.3	4420	lpp2445	2783820	2784728	p	-	unknown	3.5.2
2530.3	4419	lpp2446	2784866	2786755	p	-	unknown	1.2

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Table XIV

3602.2	5050	lpp2447	2786973	2788736	p	-	unknown	Some similarity with eukaryotic proteins	6
3601.1	5049	lpp2448	2788923	2790071	p	-	unknown	similar to sodium-proton antiporter	1.2
3600.2	5048	lpp2449	2790295	2791233	p	-	unknown	conserved hypothetical protein, some similarity with stress proteins	5.2
2453.4	4367	lpp2450	2791251	2793971	p	-	unknown	similar to cation transport ATPase	1.2
1652.4	3903	lpp2451	2794065	2794628	p	-	unknown		6
1653.3	3904	lpp2452	2794743	2795669	m	+	unknown	similar to plasminogen activator precursor from Yersinia	2.2
606.3	6327	lpp2453	2795797	2797404	m	+	unknown	Similar to amino acid transport protein	1.2
612.2	6336	lpp2454	2797735	2799900	p	-	katB catalase-peroxidase		4.2
2079.2	4153	lpp2455	2800211	2801488	m	-	unknown		6
2078.2	4152	lpp2456	2801622	2801834	m	+	unknown	hypothetical gene	6
3673.2	5098	lpp2457	2802048	2803280	m	-	unknown	Similar to major facilitator family transporter	1.2
4917.2	5899	lpp2458	2803321	2804625	m	-	SdbC proteins, putative substrate of the Dot/Icm system		5.1
4916.2	5898	lpp2459	2804894	2805778	p	-	unknown	Some similarity with eukaryotic proteins	5.2
5655.2	6237	lpp2460	2805899	2806363	m	-	unknown	Similar to bacterioferritin	4.2
5654.2	6236	lpp2461	2806763	2807122	p	-	unknown		6
4935.2	5910	lpp2462	2807250	2808320	m	-	unknown	Similar to conserved hypothetical protein	5.2
4934.3	5909	lpp2463	2808690	2809889	m	-	unknown	similar to hypothetical peptidases	2.2
5808.1	6277	lpp2464	2809944	2810516	m	-	unknown	Similar to aminoglycoside 6 -N-acetyltransferase	4.2
964.3	6563	lpp2465	2810706	2812052	m	-	unknown	C-terminal part similar to Legionella unknown virulence protein	5.1
953.2	6561	lpp2466	2812652	2814166	p	-	unknown		6
952.1	6560	lpp2467	2814143	2815063	m	-	Unknown	Similar to transcriptional regulator, LysR family	3.5.2

Table XIV

950.2	6559	lpp2468	2815247	2816761	m	-	Unknown	similar to monooxygenase	2.1.1
3252.1	4834	lpp2469	2817059	2817973	p	-	unknown		6
3251.1	4833	lpp2470	2817970	2818371	p	-	unknown	Similar to MutT/nudix family protein	3.2
901.2	6525	lpp2471	2818455	2819609	m	-	unknown		6
903.2	6526	lpp2472	2819942	2821039	p	-	unknown		5.1
905.2	6527	lpp2473	2821126	2821986	m	+	unknown		2.1.1
3250.1	4832	lpp2474	2822250	2822513	m	-	unknown	Similar to oxidoreductase	6
3249.2	4830	lpp2475	2822778	2823437	p	-	unknown		6
1562.3	3843	lpp2476	2823764	2824582	p	-	unknown		6
1560.2	3842	lpp2477	2824702	2825523	m	-	Unknown	regulatory protein (GGDEF domain)	1.3
3248.1	4829	lpp2478	2825501	2826400	m	-	unknown	similar to other proteins	5.2
3246.2	4828	lpp2479	2826758	2828743	p	-	unknown	Similar to conserved hypothetical protein	5.2
1861.3	4036	lpp2480	2828846	2829673	m	-	Unknown	Unknown	6
1860.3	4035	lpp2481	2830204	2831283	p	+	unknown	Similar to beta-lactamase precursor (Cephalosporinase)	4.2
3336.2	4882	lpp2482	2831534	2831971	p	+	unknown		6
3337.2	4883	lpp2483	2832184	2832477	m	-	unknown		6
3338.1	4884	lpp2484	2832814	2833095	p	-	unknown		6
3341.2	4886	lpp2485	2833317	2836331	p	-	unknown	Some similarities with eukaryotic proteins	5.1
3343.1	4887	lpp2486	2836545	2837183	m	-	unknown	Some similarity with eukaryotic proteins, contains a F-box domain	6
3345.2	4888	lpp2487	2837395	2839656	m	-	unknown	Some similarity with eukaryotic proteins	5.2
2585.2	4448	lpp2488	2839945	2841675	p	+	unknown		6
1567.2	3847	lpp2489	2841764	2843107	m	-	unknown		6
1566.3	3846	lpp2490	2843442	2843996	m	+	unknown		6
1664.2	3913	lpp2491	2844283	2845083	m	-	unknown		6
5297.2	6073	lpp2492	2845512	2846810	p	-	unknown		6
4519.3	5641	lpp2493	2847180	2848826	p	-	unknown	Similar to malonate decarboxylase, alpha subunit	2.1.1
979.3	6574	lpp2494	2848835	2850031	p	-	unknown	Similar to malonate decarboxylase, beta subunit	2.1.1

Table XIV

980.1	6575	lpp2495	2850032	2850751	p	-	unknown	Similar to malonate decarboxylase, gamma subunit	2.1.1
981.2	6576	lpp2496	2850748	2851371	p	-	unknown	Similar to phosphoribosyl-dephospho-CoA transferase	3.8
4517.2	5640	lpp2497	2851343	2852185	p	-	unknown	Similar to 2-(5 -triphosphoribosyl)-3 -dephosphoenzyme-A synthase	2.1.1
4819.2	5845	lpp2498	2852182	2853129	p	-	unknown	Similar to malonyl-CoA acyl-carrier-protein transacylase	2.1.1
4821.2	5847	lpp2499	2853263	2854156	p	-	unknown	Similar to phosphatase	2.6
4850.2	5860	lpp2500	2854334	2856118	p	-	unknown		6
4851.2	5861	lpp2501	2856394	2856879	p	-	unknown	Similar to conserved hypothetical protein	5.2
2347.2	4291	lpp2502	2856906	2857949	p	+	unknown		6
2346.1	4290	lpp2503	2857986	2858366	p	+	unknown	putative membrane protein	6
2345.2	4289	lpp2504	2858473	2858901	m	+	unknown		6
1336.3	3709	lpp2505	2859132	2860247	m	-	unknown	Similar to florfenicol efflux pump-like protein	1.2
2321.3	4275	lpp2506	2860589	2861140	m	-	unknown	similar to conserved hypothetical protein	5.2
5412.1	6120	lpp2507	2861289	2862248	p	-	unknown	Similar to conserved hypothetical protein	5.2
4591.2	5689	lpp2508	2862286	2862759	p	-	unknown	similar to hypothetical proteins	5.2
4590.1	5688	lpp2509	2862859	2863269	p	-	unknown		5.2
4589.1	5686	lpp2510	2863393	2863932	m	-	unknown		6
4588.2	5685	lpp2511	2864177	2864728	m	-	unknown		6
4587.2	5684	lpp2512	2864938	2865423	p	+	unknown		6
5413.1	6121	lpp2513	2865508	2865786	p	-	unknown		6
2419.3	4341	lpp2514	2865969	2866649	p	-	unknown	Similar to D-alanyl-D-alanine dipeptidase	1.1
2418.2	4340	lpp2515	2866732	2867460	p	+	unknown	predicted integral membrane protein	5.2
2415.2	4339	lpp2516	2867540	2868508	m	-	unknown	Similar to N-hydroxyarylamine O-acetyltransferase	2.1.1
4170.1	5413	lpp2517	2868667	2871432	m	-	unknown	Ankyrin repeat protein	6
4168.2	5411	lpp2518	2871656	2872150	p	-	unknown		6
4780.2	5818	lpp2519	2872198	2872647	m	-	unknown		6

Table XIV

4779.1	5817	lpp2520	2872970	2873416	p	-	unknown	Similar to unknown protein	5.2
4778.1	5816	lpp2521	2873577	2874206	p	-	unknown	ankyrin repeat protein	6
4777.2	5815	lpp2522	2874405	2875712	p	-	unknown	Similar to two-component response regulator	6
5417.1	6122	lpp2523	2875837	2876244	m	-	unknown	Similar to two-component sensor	3.5.2
4357.3	5537	lpp2524	2876308	2877585	m	-	shkA	histidine kinase	1.3
4358.2	5538	lpp2525	2877578	2878132	m	-	unknown	Similar to guanylate cyclase-related protein	2.3
5586.1	6201	lpp2526	2878357	2878740	m	-	unknown		6
2485.3	4390	lpp2527	2878902	2879519	p	-	unknown		6
1878.3	4046	lpp2528	2879724	2880656	p	-	unknown	Similar to hypothetical protein	5.2
1875.2	4045	lpp2529	2880843	2882006	p	+	unknown	Similar to major facilitator superfamily transporters	1.2
4363.2	5539	lpp2530	2882145	2882864	p	-	unknown	Similar to aspartyl/asparaginyl beta-hydroxylase	3.8
5076.2	5995	lpp2531	2882924	2883403	m	-	unknown	Similar to hydrogenase 1 maturation protease	3.8
5077.3	5996	lpp2532	2883400	2884692	m	-	unknown	Similar to coenzyme F420-reducing hydrogenase, alpha subunit	1.4
3652.2	5082	lpp2533	2884685	2885470	m	-	unknown	Similar to coenzyme F420-reducing hydrogenase, gamma subunit	1.4
3651.1	5081	lpp2534	2885488	2886333	m	-	unknown	Similar to 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	1.4
3650.1	5080	lpp2535	2886326	2887465	m	-	unknown	Similar to hydrogenase subunit	1.4
2506.2	4403	lpp2536	2887501	2888559	m	-	Hydrogenase expression/formation protein HypE		1.4
2508.3	4404	lpp2537	2888556	2889662	m	-	Hydrogenase expression/formation protein HypD		1.4
3647.2	5078	lpp2538	2889659	2889886	m	-	Hydrogenase expression/formation protein HypC		1.4
1320.3	3698	lpp2539	2889896	2892121	m	-	Hydrogenase maturation protein HypF		1.4

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1394.2	3741	lpp2557	2910430	2910879	m	-	unknown	similar to hypothetical Inosine-5 - monophosphate dehydrogenase	2.3
1396.3	3742	lpp2558	2911010	2911996	p	-	unknown	Similar to alcohol dehydrogenase	2.1.1
1397.2	3743	lpp2559	2912258	2912752	p	-	unknown	Similar to small heat shock protein	4.1
3811.1	5179	lpp2560	2912801	2913304	m	-	unknown	Predicted membrane protein	6
3810.1	5178	lpp2561	2913574	2914266	p	-	unknown	Similar to conserved hypothetical protein	5.2
1807.3	4007	lpp2562	2914317	2915735	m	-	unknown	Similar to homoserimidine synthase	2.2
1806.2	4006	lpp2563	2916013	2916462	p	-	unknown	Similar to rRNA methylase	3.6
1805.3	4005	lpp2564	2916620	2917273	m	-	unknown	Similar to thiamin pyrophosphokinase	2.5
4551.2	5663	lpp2565	2917254	2917520	m	-	unknown	Similar to conserved hypothetical protein	5.2
4552.4	5664	lpp2566	2917788	2918696	p	-	unknown		6
5354.3	6096	lpp2567	2919033	2919257	p	+	unknown		6
1467.5	3785	lpp2568	2919387	2919959	p	-	unknown	Similar to conserved hypothetical protein	5.2
1466.2	3784	lpp2569	2919999	2920739	p	-	unknown	similar to carbonic anhydrase	4.7
4645.2	5721	lpp2570	2920824	2922056	p	-	unknown	similar to multidrug resistance protein, MFS superfamily	1.2
4644.3	5720	lpp2571	2922053	2923318	m	-	unknown	Similar to hypothetical protein	5.2
4206.2	5436	lpp2572	2923626	2926454	p	-	unknown		6
4205.2	5435	lpp2573	2926474	2927346	p	-	unknown		6
4203.2	5434	lpp2574	2927752	2929014	p	-	unknown	similar to sensor histidine kinase/response regulator	1.3
4200.2	5433	lpp2575	2929062	2929757	m	-	unknown		6
1377.5	3730	lpp2576	2930154	2932577	m	-	unknown		6
1378.5	3731	lpp2577	2932649	2933797	m	-	sdeD	SdeD protein (substrate of the Dot/Icm system)	5.1
5349.3	6095	lpp2578	2934089	2936779	p	-	sdCA	SdCA protein, paralog of Dot/Icm system)	5.1
4431.2	5586	lpp2579	2936942	2939656	p	-	sidC	SidC protein (substrate of the Dot/Icm system)	5.1
5129.4	6016	lpp2580	2939975	2943127	m	+	lmxF	Similar to multidrug efflux pump	1.2

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4873.3	5873	lpp2581	2943187	2944341	m	-	ImxE	unknown	Similar to efflux protein	1.2
4872.3	5872	lpp2582	2944347	2945909	m	+	lprN	unknown	Similar to outer membrane efflux protein	1.2
6086.1	6331	lpp2583	2946091	2946405	m	-		unknown	Major facilitator superfamily (MFS) transporter	5.1
5685.2	6246	lpp2584	2946460	2947692	m	-	smIA	unknown	Similar to transcriptional regulator (Lrp family)	5.1
5686.2	6247	lpp2585	2947892	2948365	p	-		unknown		3.5.2
5687.1	6248	lpp2586	2948562	2948903	p	-		unknown		6
5688.2	6249	lpp2587	2949093	2949653	p	-		unknown		6
5569.1	6195	lpp2588	2949746	2950114	m	+		Unknown		6
5566.1	6194	lpp2589	2950336	2950515	p	+		Unknown		6
1065.3	3549	lpp2590	2950556	2951686	m	-		unknown	similar to other protein	5.2
1063.1	3548	lpp2591	2952111	2953355	m	-		unknown		6
4998.2	5943	lpp2592	2953818	2955437	m	-		unknown		6
4995.2	5942	lpp2593	2955658	2957208	p	-		unknown	weakly similar to alpha-glucosidase	2.1.1
3316.1	4870	lpp2594	2957609	2959303	m	-		unknown		6
2057.3	4140	lpp2595	2960106	2961149	p	-	aroF	phospho-2-dehydro-3-deoxyheptonate aldolase		
977.3	6573	lpp2596	2961146	2961730	p	-		unknown	similar to chorismate mutase (N-terminal part)	2.2
976.3	6572	lpp2597	2961764	2962024	p	-		unknown	similar to chorismate mutase (C-terminal part)	2.2
974.2	6571	lpp2598	2962024	2963190	p	-	aspB	unknown	Similar to aspartate aminotransferase	2.2
2056.1	4139	lpp2599	2963368	2964264	p	-		unknown	Similar to tellurite resistance protein TehB	4.2
1270.3	3669	lpp2600	2964297	2964728	m	-		unknown	similar to unknown protein similar to hemoglobin (protozoan/cyanobacterial globin family)	5.2
1271.4	3670	lpp2601	2964808	2965182	p	-		unknown		1.4
1272.5	3671	lpp2602	2965179	2966135	p	-		unknown	similar to xylene monooxygenase	2.1.1
2054.2	4138	lpp2603	2966360	2967379	p	-		unknown	Similar to conserved hypothetical protein	5.2
3319.1	4871	lpp2604	2967503	2968849	m	-		unknown		6
4962.2	5925	lpp2605	2969502	2969909	m	-		unknown		6

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4961.1	5924	lpp2606	2970108	2970491	m	-	unknown	Similar to large conductance mechanosensitive channel protein	1.2
4960.2	5923	lpp2607	2970606	2971433	m	-	unknown		6
4943.2	5914	lpp2608	2971714	2972139	m	-	unknown		6
4942.1	5913	lpp2609	2972273	2972482	m	-	unknown		6
4941.3	5912	lpp2610	2972499	2972939	m	-	unknown		6
748.4	6435	lpp2611	2973586	2974959	p	-	unknown	similar to membrane-bound lytic murein transglycosylase A	1.1
749.1	6436	lpp2612	2975335	2975625	p	-	unknown		6
750.2	6437	lpp2613	2975856	2976002	m	-	unknown	hypothetical gene	6
752.2	6438	lpp2614	2976101	2976256	m	-	unknown	hypothetical gene	6
2143.5	4186	lpp2615	2976501	2977898	m	-	unknown		6
2302.2	4265	lpp2616	2978085	2978420	m	-	unknown	similar to protein secretion chaperonin CsaA	1.6
1182.3	3620	lpp2617	2978430	2979344	m	-	unknown	Predicted transmembrane protein	5.2
1180.2	3619	lpp2618	2979410	2980165	m	-	unknown	Similar to transcriptional regulator, AraC family	3.5.2
1179.1	3617	lpp2619	2980423	2981019	m	+	unknown		6
2712.1	4515	lpp2620	2981450	2982223	m	-	unknown		6
2713.2	4516	lpp2621	2982430	2983425	m	-	unknown	Similar to permeases of the drug/metabolite transporter (DMT) superfamily	1.2
2717.1	4517	lpp2622	2983872	2985539	m	-	unknown	putative membrane protein	6
2718.1	4518	lpp2623	2985717	2987084	p	-	unknown	Similar to hexose phosphate transport protein	1.2
2477.1	4384	lpp2624	2987347	2987829	p	-	unknown	Similar to N-terminal part of rare lipoprotein A	1.2
2479.2	4385	lpp2625	2988299	2989141	m	-	unknown		6
1324.4	3701	lpp2626	2989724	2991112	p	-	Unknown	similar to eukaryotic serine threonine protein kinase	3.8
2073.4	4150	lpp2627	2991137	2991820	m	-	unknown	Similar to Legionella putative transcriptional regulator	3.5.2
1386.3	3734	lpp2628	2992329	2992706	m	-	unknown	Similar to conserved hypothetical protein	5.2
1385.2	3733	lpp2629	2993009	2993734	m	-	unknown		6
2075.1	4151	lpp2630	2993857	2994111	m	-	unknown		6

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3446.1	4945	lpp2650	3017091	3018176	p	-	unknown	similar to E. coli Smf protein	5.2
3447.1	4946	lpp2651	3018166	3018603	p	-	unknown	similar to unknown protein	5.2
5200.2	6037	lpp2652	3018683	3020962	p	-	topA	DNA topoisomerase I	3.4
3271.3	4844	lpp2653	3021173	3023146	m	-	unknown	similar to membrane bound acyltransferase	2.1.1
3272.1	4845	lpp2654	3023282	3023722	m	-	unknown	Similar to conserved hypothetical protein	5.2
3273.1	4846	lpp2655	3023853	3024275	p	-	unknown	Similar to hypothetical protein	5.2
3275.1	4847	lpp2656	3024356	3025597	p	-	unknown	6	6
3277.2	4848	lpp2657	3025898	3026695	p	-	unknown	Similar to unknown protein	5.2
3278.1	4849	lpp2658	3026750	3027166	m	-	unknown	6	6
3280.1	4851	lpp2659	3027281	3028132	m	-	unknown	Similar to unknown protein	5.2
637.3	6374	lpp2660	3028286	3030322	m	-	unknown	Similar to peptidase	2.2
636.2	6372	lpp2661	3030466	3031380	m	-	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine	
635.5	6371	lpp2662	3031628	3032824	m	-	ftsZ	deacetylase	2.4
3282.3	4852	lpp2663	3033019	3034257	m	-	ftsA	Cell division protein FtsZ ATP-binding cell division protein FtsA	1.7
3283.1	4853	lpp2664	3034257	3034976	m	-	ftsQ	Cell division protein FtsQ	1.7
1463.2	3783	lpp2665	3034992	3036086	m	-	ddlA	D-alanine--D-alanine ligase A	1.1
1461.3	3782	lpp2666	3036070	3036981	m	-	murB	UDP-N-acetylenolpyruvoylglucosamine reductase	1.1
2358.3	4300	lpp2667	3037005	3038414	m	-	murC	UDP-N-acetylmutarinate--L-alanine ligase	1.1
1701.6	3935	lpp2668	3038424	3039599	m	+	ftsW	Cell division protein ftsW	1.7
1699.7	3934	lpp2669	3039605	3040948	m	-	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.1
3694.3	5112	lpp2670	3040962	3042047	m	-	mraY	Phospho-N-acetylmuramoyl-pentapeptide-transferase	1.1

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683.2	6402	lpp2671	3042162	3043499	m	+	murF	UDP-N-acetyl/muramoyl-tripeptide--D-alanyl-D-alanine ligase unknown	Similar to cell division protein	1.1
684.5	6403	lpp2672	3043740	3044519	m	-		unknown	similar to chromosome partition protein smc	1.7
3697.5	5113	lpp2673	3044524	3048018	m	-	smc	unknown	Similar to acid phosphatase, class B	3.4
3150.1	4770	lpp2674	3048193	3048873	p	+		unknown		2.6
3149.1	4768	lpp2675	3048975	3050036	m	+		unknown	Weakly similar to cysteine protease	2.2
3148.1	4767	lpp2676	3050346	3051158	p	+		unknown	Similar to hypothetical protein	5.2
3147.1	4766	lpp2677	3051232	3051714	m	-	greA	transcription elongation factor GreA		3.5.3
727.3	6423	lpp2678	3051723	3054926	m	+	carB	carbamoyl-phosphate synthase large subunit		2.3
2098.2	4161	lpp2679	3055055	3055327	m	-		unknown		6
2095.2	4160	lpp2680	3055440	3056621	p	-		unknown	Similar to conserved hypothetical protein	5.2
3146.2	4765	lpp2681	3056661	3057413	m	-		unknown	Similar to hypothetical protein	5.2
880.3	6508	lpp2682	3057413	3058483	m	-		unknown	Putative membrane protein	5.2
881.2	6509	lpp2683	3058480	3059559	m	+		unknown	Predicted membrane protein, similar to putative permease	5.2
882.3	6510	lpp2684	3059763	3061214	p	-	pepA	unknown	Similar to leucine aminopeptidase	3.8
2221.3	4225	lpp2685	3061195	3061629	p	-	holC	unknown	Similar to DNA polymerase III, chi subunit	3.1
4373.3	5547	lpp2686	3061776	3062093	m	-		unknown	Similar to hypothetical protein	5.2
2542.2	4424	lpp2687	3062116	3063480	m	-		unknown	Similar to aminopeptidase	2.2
4374.4	5548	lpp2688	3063485	3065056	m	-		unknown	similar to integral membrane protein MviN	5.2
5806.2	6275	lpp2689	3065414	3065680	p	-	rpst	30S ribosomal subunit protein S20		3.7.1
4818.3	5844	lpp2690	3065741	3066952	m	-		unknown		6
4817.4	5843	lpp2691	3067304	3068686	m	-		unknown		6
4167.4	5410	lpp2692	3069093	3072695	m	+	enhC	enhanced entry protein EnhC		4.6
4165.1	5409	lpp2693	3072722	3073288	m	+	enhB	enhanced entry protein EnhB		4.6

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4164.1	5408	lpp2694	3073285	3074007	m	+	enhA	enhanced entry protein EnhA		4.6
4162.2	5407	lpp2695	3074180	3076687	p	-		Unknown	regulatory protein (GGDEF and EAL domains)	1.3
628.3	6361	lpp2696	3076956	3077615	p	+		unknown		6
627.1	6358	lpp2697	3077783	3078931	p	-		Unknown	similar to putative protein from Stx2 converting bacteriophage I	4.5
2217.3	4222	lpp2698	3078955	3080811	m	-	uvrC	unknown	similar to excinuclease ABC subunit C	3.2
1511.3	3812	lpp2699	3080823	3081482	m	-	gacA/letA	Legionella transmission activator LetA		3.5.2
1510.3	3811	lpp2700	3081607	3082425	m	-	phhA	unknown	similar to phenylalanine-4- hydroxylase	2.2
1508.4	3809	lpp2701	3082865	3083962	p	-		unknown	belong to the CinA protein family	5.2
3385.1	4903	lpp2702	3083921	3084946	m	-	obgL	unknown	Similar to Legionella essential GTPase	2.3
3386.1	4904	lpp2703	3085160	3085438	m	-	rpmA	50S ribosomal protein L27		3.7.1
1894.2	4058	lpp2704	3085451	3085762	m	-	rplU	50S ribosomal protein L21		3.7.1
1893.2	4057	lpp2705	3086005	3086664	p	-		unknown	similar to 50S ribosomal subunit protein L25, RplY	3.7.1
2253.2	4240	lpp2706	3086781	3087350	p	-	pth	unknown	similar to peptidyl-tRNA hydrolase	3.7.5
2252.1	4239	lpp2707	3087369	3088460	p	-		unknown	Similar to GTP-binding protein	4.6
3388.1	4905	lpp2708	3088822	3089937	p	-		Unknown	regulatory protein (GGDEF domain)	1.3
3389.1	4906	lpp2709	3090071	3091039	p	-	ispB	unknown	similar to octaprenyl-diphosphate synthase	2.5
3390.1	4908	lpp2710	3091066	3091281	m	-		unknown	hypothetical gene	6
3391.2	4909	lpp2711	3091262	3093517	m	-	feoB	ferrous iron transporter B		1.2
5180.1	6029	lpp2712	3093514	3093741	m	-	feoA	ferrous iron transporter A		1.2
3544.2	5010	lpp2713	3093830	3094912	m	-		unknown	similar to predicted ATPase	5.2
3543.1	5009	lpp2714	3094909	3095571	m	-		unknown	similar to unknown protein	5.2

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3542.1	5008	lpp2715	3095808	3096596	p	-	panB	unknown	similar to 3-methyl-2-oxobutanatehydroxymethyltransferase	2.5
3541.1	5007	lpp2716	3096608	3097366	p	-	panC	unknown	similar to pantothenate synthetases	2.5
307.2	4722	lpp2717	3097363	3097896	p	-		unknown	Similar to conserved hypothetical proteins	5.2
306.1	4715	lpp2718	3097910	3099325	m	-		unknown	Similar to biotin carboxylase (A subunit of acetyl-CoAcarboxylase)	2.4
305.2	4709	lpp2719	3099318	3100034	m	-		unknown	Similar to diene lactone hydrolase family protein	2.1.1
1724.4	3950	lpp2720	3100316	3101182	p	-		unknown	similar to unknown protein	5.2
1725.4	3951	lpp2721	3101317	3102171	m	-	rpoH	RNA polymerase sigma-32 factor		3.7.3
4294.3	5490	lpp2722	3102467	3103396	m	-	ftsX	unknown	Similar to cell division ABC transporter, permease protein FtsX	1.7
2337.3	4284	lpp2723	3103390	3104040	m	-	ftsE	unknown	Highly similar to cell division ABC transporter, ATP-binding protein FtsE	1.7
2339.4	4285	lpp2724	3104027	3105094	m	-		unknown	Similar to C-terminal part of signal recognition particle GTPase, FtsY	1.7
4295.3	5491	lpp2725	3105157	3106482	p	-		unknown	Similar to zinc protease	2.2
4296.1	5492	lpp2726	3106479	3107783	p	-		unknown	Similar to zinc protease	2.2
4297.2	5493	lpp2727	3107780	3108325	p	-		unknown	Similar to methyltransferase proteins	3.2
5178.1	6028	lpp2728	3108400	3108891	p	+	dotD	lipoprotein DotD		1.6
2362.3	4303	lpp2729	3108872	3109783	p	+	dotC	defect in organelle trafficking lipoprotein DotC		1.6
2364.1	4304	lpp2730	3109783	3110916	p	-	dotB	defect in organelle trafficking protein DotB (ATPase)		1.6
2365.2	4305	lpp2731	3110998	3112725	p	+		unknown	Similar to 5'-nucleotidase, catalytic domain	2.3
1720.3	3947	lpp2732	3112767	3113564	m	-		unknown	similar to unknown protein	5.2
3538.1	5004	lpp2733	3113594	3114538	m	-		unknown	similar to oxidoreductase	2.1.1

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1277.2	3674	lpp2734	3114775	3115797	p	-	unknown	similar to D-alanine-D-alanine ligase (N-terminal part) similar to aldolase	2.2
1275.2	3673	lpp2735	3116071	3116958	p	-	unknown	Similar to hypothetical protein	2.1.1
1273.4	3672	lpp2736	3117097	3117804	p	-	unknown		5.2
3540.2	5006	lpp2737	3117791	3119638	p	-	dlpA	DlpA protein (isocitrate and isopropylmalate dehydrogenases family protein)	
3582.2	5033	lpp2738	3119638	3120498	p	-		similar to hypothetical protein	2.1.1
3581.1	5032	lpp2739	3120759	3121475	m	-	sbpA	small basic protein SbpA	5.2
1770.2	3979	lpp2740	3121606	3124713	m	+	dotA	defect in organelle trafficking protein DotA	
1772.1	3980	lpp2741	3124710	3125165	m	-	icmV	intracellular multiplication protein IcmV	1.6
1773.1	3981	lpp2742	3125278	3125733	p	-	icmW	Intracellular multiplication protein IcmW	1.6
1774.2	3982	lpp2743	3125733	3127151	p	+	icmX	Intracellular multiplication protein IcmX	
3578.3	5031	lpp2744	3127158	3128798	m	-	lphB	unknown, LphB	1.6
3846.2	5200	lpp2745	3129165	3131708	p	-		similar to cation transport ATPase	5.2
273.1	4525	lpp2746	3131959	3132489	p	-			1.2
271.1	4514	lpp2747	3132561	3133361	m	-		Similar to SAM dependent methyltransferase	6
270.1	4507	lpp2748	3133485	3134315	m	-		Similar to eukaryotic phytanoyl-CoA dioxygenase	4.6
269.1	4501	lpp2749	3134430	3135479	m	-		similar to glycosyltransferase	2.4
268.1	4495	lpp2750	3135460	3135654	m	-		similar to unknown proteins	1.1
267.3	4490	lpp2751	3135677	3136618	m	+	miaA	similar to tRNA delta(2)-isopentenylpyrophosphate transferase	5.2
5232.2	6051	lpp2752	3136611	3138341	m	-	mutL	DNA mismatch repair protein MutL	3.6
123.2	3647	lpp2753	3138332	3139762	m	+		similar to N-acetylmuramoyl-L-alanine amidase	3.2
							unknown		1.1

Table XIV

124.1	3652	lpp2754	3139759	3140241	m	-	unknown	similar to conserved hypothetical protein	5.2
125.2	3657	lpp2755	3140367	3141848	m	-	unknown	similar to conserved hypothetical protein	5.2
2021.1	4122	lpp2756	3141976	3142371	m	-	sspB	similar to stringent starvation protein B	4.1
2020.1	4121	lpp2757	3142374	3142994	m	-	sspA	similar to stringent starvation protein A	4.1
2019.2	4119	lpp2758	3143242	3143988	m	+	petC	similar to ubiquinol--cytochrome c oxydoreductase, cytochrome c1	1.4
698.2	6410	lpp2759	3143985	3145199	m	-	petB	Similar to ubiquinol--cytochrome c reductase, cytochrome b	1.4
697.1	6409	lpp2760	3145210	3145827	m	+	petA	Similar to ubiquinol--cytochrome c reductase, iron-sulfur subunit	1.4
696.2	6408	lpp2761	3146001	3146432	m	-	rpsI	30S ribosomal subunit protein S9	3.7.1
5229.1	6049	lpp2762	3146438	3146872	m	-	rplM	50S ribosomal subunit protein L13	3.7.1
4856.2	5863	lpp2763	3147212	3147529	m	-		similar to putative ferredoxin-2fe-2s protein	1.4
4855.2	5862	lpp2764	3147531	3147824	m	-	himA	Similar to integration host factor, alpha subunit	3.4
2407.3	4332	lpp2765	3147827	3150208	m	-	pheT	Phenylalanyl-tRNA synthetase, beta subunit	3.7.2
4503.1	5632	lpp2766	3150466	3151482	m	-	pheS	Phenylalanyl-tRNA synthetase, alpha subunit	3.7.2
4505.3	5633	lpp2767	3151619	3151978	m	-	rplT	50S ribosomal protein L20	3.7.1
5227.2	6048	lpp2768	3151994	3152194	m	-	rpmI	50S ribosomal protein L35	3.7.1
5226.2	6047	lpp2769	3152215	3152751	m	-	infC	Translation initiation factor IF-3	3.7.3
4923.2	5904	lpp2770	3152776	3154689	m	-	thrS	Threonyl tRNA synthetase	3.7.2
5225.1	6046	lpp2771	3154938	3155150	m	-		unknown	6
								hypothetical gene	

Table XIV

3516.2	4989	lpp2772	3155205	3155492	p	-	unknown	Similar to conserved hypothetical protein	5.2
3515.2	4988	lpp2773	3155827	3156312	p	-	unknown		6
3514.1	4987	lpp2774	3156327	3156569	p	-	unknown	hypothetical gene	6
3512.1	4986	lpp2775	3156958	3158520	m	-	unknown		6
3511.2	4985	lpp2776	3158801	3159952	p	-	unknown	similar to conserved hypothetical protein	5.2
3509.2	4983	lpp2777	3159931	3160962	p	-	unknown	Putative cAMP/cGMP binding protein	5.2
2590.3	4450	lpp2778	3160969	3161886	p	-	unknown	Similar to unknown protein	5.2
2591.3	4451	lpp2779	3162014	3163069	m	-	unknown	Similar to NADH-dependent flavin oxidoreductase (Oye family)	1.4
3508.2	4982	lpp2780	3163141	3163440	m	-	unknown	Similar to transcriptional regulator, ArsR family	3.5.2
3507.1	4981	lpp2781	3163693	3164037	m	-	unknown	Some similarity with eukaryotic proteins	6
3506.1	4980	lpp2782	3164154	3164783	p	-	unknown	similar to membrane protein	5.2
3504.1	4979	lpp2783	3164993	3165487	m	-	Peptidyl-prolyl cis-trans isomerase B (cyclophilin-type PPIase family)		
3503.2	4978	lpp2784	3165514	3166665	m	-	unknown	Similar to queuine tRNA-ribosyltransferase	3.8
3502.3	4977	lpp2785	3166727	3167218	m	+	unknown	Similar to disulfide bond formation protein DsbB	3.6
5804.1	6274	lpp2786	3167215	3167643	m	+	unknown	Similar to cytochrome c5	3.9
1517.3	3816	lpp2787	3167832	3169082	p	-	unknown	similar to 2-amino-3-ketobutyrate coenzyme A ligase	1.4
1519.2	3817	lpp2788	3169163	3170188	m	-	unknown	Putative response regulator	2.2
1521.2	3819	lpp2789	3170469	3171032	p	-	unknown	Putative membrane protein	3.5.2
4415.3	5577	lpp2790	3171120	3172409	m	-	unknown	Similar to signal transduction histidine kinase	5.2
4325.3	5510	lpp2791	3172800	3173729	p	-	hemC	Porphobilinogen deaminase	1.3
4326.1	5511	lpp2792	3173726	3174478	p	-	hemD	Uroporphyrinogen-III synthetase	2.5
4327.1	5512	lpp2793	3174482	3175606	p	-	hemX	Similar to uroporphyrinogen III methylase HemX	2.5

Table XIV

3917.1	5238	lpp2817	3207607	3207882	m	-	rpsO	30S ribosomal protein S15	3.7.1
3919.1	5239	lpp2818	3208030	3208941	m	-	truB	trRNA pseudouridine synthase B	3.6
3920.1	5240	lpp2819	3208928	3209299	m	-	rbfA	Ribosome-binding factor A	3.7.3
1730.3	3953	lpp2820	3209303	3211909	m	-	infB	Translation initiation factor IF-2	3.7.3
3621.2	5062	lpp2821	3211998	3213476	m	-	nusA	Transcription elongation protein nusA	3.5.3
3619.1	5061	lpp2822	3213488	3213946	m	-		unknown	Similar to conserved hypothetical protein
1400.2	3746	lpp2823	3214187	3215626	m	-	nuoN	NADH dehydrogenase I chain N	5.2
1402.2	3747	lpp2824	3215683	3217188	m	-	nuoM	NADH-quinone oxidoreductase chain M	1.4
3618.2	5060	lpp2825	3217204	3219177	m	+	nuoL	NADH-quinone oxidoreductase chain L	1.4
3617.2	5059	lpp2826	3219182	3219487	m	-	nuoK	NADH-quinone oxidoreductase chain K	1.4
1006.3	3514	lpp2827	3219505	3220164	m	+	nuoJ	NADH-quinone oxidoreductase chain J	1.4
1009.2	3515	lpp2828	3220176	3220676	m	-	nuoI	NADH-quinone oxidoreductase chain I	1.4
1010.2	3516	lpp2829	3220695	3221717	m	-	nuoH	NADH-quinone oxidoreductase chain H	1.4
1011.5	3517	lpp2830	3221730	3224081	m	-	nuoG	NADH dehydrogenase I chain G	1.4
291.4	4618	lpp2831	3224098	3225375	m	-	nuoF	NADH dehydrogenase I chain F	1.4
292.1	4625	lpp2832	3225394	3225861	m	-	nuoE	NADH dehydrogenase I chain E	1.4
293.2	4632	lpp2833	3225958	3227211	m	-	nuoD	NADH dehydrogenase I chain D	1.4
294.1	4637	lpp2834	3227204	3227887	m	-	nuoC	NADH dehydrogenase I chain C	1.4
295.1	4642	lpp2835	3227910	3228386	m	-	nuoB	NADH dehydrogenase I chain B	1.4
296.1	4650	lpp2836	3228633	3228989	m	+	nuoA	NADH dehydrogenase I chain A	1.4

Table XIV

297.2	4661	lpp2837	3229169	3229492	m	-	secG	Protein-export membrane protein secG (Preprotein translocase subunit)	1.6	
5719.2	6259	lpp2838	3229480	3230229	m	-	tpi	triosephosphate isomerase	2.1.2	
5266.2	6062	lpp2839	3230473	3233832	p	-	lepA	effector protein A, substrate of the Dot/Icm secretion system	5.1	
633.3	6370	lpp2840	3233902	3235269	m	-	msrA	unknown	2.1.1	
632.2	6367	lpp2841	3235333	3236127	m	-	folP	Dihydropteroate synthase	2.5	
3201.1	4801	lpp2842	3236241	3238160	m	+	ftsH	Cell division protease ftsH	1.7	
666.2	6392	lpp2843	3238274	3238894	m	-	rrmJ	Ribosomal RNA large subunit methyltransferase (Cell division protein FtsJ)	3.6	
665.2	6391	lpp2844	3238997	3239263	p	-		unknown	Similar to predicted RNA-binding protein	4.6
663.2	6390	lpp2845	3239314	3241290	m	-		unknown	Similar to O-acetyltransferase	1.1
3199.1	4800	lpp2846	3241478	3243205	p	-	frgA	FrgA protein	5.2	
3198.1	4799	lpp2847	3243465	3244025	p	-		unknown	Similar to phosphatidylglycerophosphate synthase	2.4
2322.2	4276	lpp2848	3244022	3244714	p	-		unknown	Similar to DnaA, ATPase involved in DNA replication initiation	3.1
2323.2	4277	lpp2849	3244997	3245797	p	-		unknown	Similar to putative coproporphyrinogen oxidase A	5.1
2324.5	4278	lpp2850	3245682	3246995	m	-		unknown	6	
3196.3	4798	lpp2851	3247256	3248758	m	-		unknown	Predicted membrane protein, similar to transporters	1.2
2151.2	4194	lpp2852	3248826	3250208	m	-		unknown	6	
532.2	6085	lpp2853	3250346	3251458	p	+		unknown	Similar to conserved hypothetical protein	5.2
533.2	6089	lpp2854	3251508	3252305	m	-	aroE	shikimate 5-dehydrogenase	2.2	
536.3	6098	lpp2855	3252529	3255126	m	-	pepN	aminopeptidase N	2.2	

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1454.2	3778	lpp2856	3255293	3257224	p	-	unknown	Similar to conserved hypothetical protein	5.2
1905.2	4065	lpp2857	3257378	3258643	p	-	unknown	Similar to conserved hypothetical protein	5.2
1906.2	4066	lpp2858	3258640	3260163	p	-	unknown	similar to unknown protein	5.2
220.1	4215	lpp2859	3260558	3261250	m	-	unknown	Similar to conserved hypothetical protein	5.2
221.1	4220	lpp2860	3261250	3262149	m	-	unknown	Similar to dihydrodipicolinate synthase	2.2
222.1	4223	lpp2861	3262142	3262621	m	-	unknown	Similar to hypothetical protein	5.2
223.1	4227	lpp2862	3262734	3263612	p	-	unknown	Similar to transcriptional regulator	3.5.2
5822.1	6282	lpp2863	3263771	3263935	m	-	unknown		6
3466.1	4957	lpp2864	3263922	3264122	m	-	unknown	similar to resolvase (partial)	4.5
226.4	4242	lpp2865	3264230	3265090	p	-	unknown		6
5823.2	6283	lpp2866	3265171	3266376	m	+	unknown	Similar to aminopeptidase	2.2
2924.3	4627	lpp2867	3266557	3268539	p	+	unknown	Putative membrane protein	6
2925.1	4628	lpp2868	3268623	3270620	m	-	rep	ATP-dependent DNA helicase Rep	
2926.1	4629	lpp2869	3270679	3270828	m	-	unknown	hypothetical gene	3.1
									6
2928.2	4630	lpp2870	3271036	3271881	p	-	unknown	Similar to disulfide bond chaperones of the HSP33 family	3.9
2929.1	4631	lpp2871	3271895	3272392	m	-	unknown	Similar to hypothetical protein	5.2
753.2	6439	lpp2872	3272659	3273618	m	+	unknown	Similar to conserved hypothetical protein	5.2
754.2	6440	lpp2873	3273796	3274806	p	-	unknown	Similar to predicted oxidoreductase	2.1.1
755.3	6441	lpp2874	3274914	3275726	p	-	unknown	similar to unknown protein	5.2
2604.3	4460	lpp2875	3275838	3277664	p	-	typA	Similar to GTP-binding protein TypA/BipA	3.7.4
2602.2	4459	lpp2876	3277671	3278558	p	-	unknown	Similar to probable inorganic polyphosphate/ATP-NAD kinase	2.5
2412.2	4336	lpp2877	3278562	3280229	p	-	recN	DNA repair protein recN	3.2
2413.1	4337	lpp2878	3280385	3280591	p	-	unknown	Similar to cold shock protein CspC	4.1
2414.2	4338	lpp2879	3280794	3281861	p	-	unknown	Similar to efflux protein	1.2
2932.3	4633	lpp2880	3281866	3284910	p	-	unknown	similar to unknown protein	5.2

Table XIV

2933.2	4634	lpp2881	3284999	3285910	p	-	unknown	Similar to conserved hypothetical protein	5.2
2934.1	4635	lpp2882	3286057	3287313	p	-	unknown		6
2938.4	4636	lpp2883	3287380	3291033	m	sidH	substrate of the Legionella pneumophila Dot/Icm system, truncated C-terminal part		5.2
616.5	6340	lpp2884	3291076	3292122	p	-	Unknown	Similar to transposase (IS21 family)	4.5
591.4	6304	lpp2885	3292119	3292913	p	-	Unknown	Similar to transposase (IS21 family)	4.5
590.4	6299	lpp2886	3292962	3296060	m	sidH	substrates of the Legionella pneumophila Dot/Icm system, truncated N-terminal part		5.2
5656.2	6238	lpp2887	3296181	3296903	m	-	unknown	conserved ubiquitin conjugation factor E4 family domain (U-box)	5.2
5668.2	6240	lpp2888	3297191	3299038	p	-	unknown		6
5669.2	6241	lpp2889	3299095	3300735	m	-	unknown		6
5671.2	6242	lpp2890	3300732	3301112	m	-	unknown	Similar to acyl-CoA hydrolase	2.4
719.4	6420	lpp2891	3301115	3303484	m	-	unknown	Similar to transcriptional accessory protein	3.5.2
722.3	6421	lpp2892	3303608	3304273	m	-	unknown	Similar to thiopurine S-methyltransferase	2.3
723.3	6422	lpp2893	3304270	3306084	m	-	Glucosamine--fructose-6-phosphate aminotransferase		2.1.1
4266.3	5472	lpp2894	3306449	3307750	m	-	unknown	Similar to lysophospholipase A	2.4
6285.1	6362	lpp2895	3307993	3309078	p	-	Unknown	Similar to transposase (IS4 family)	4.5
5337.1	6090	lpp2896	3309104	3309397	p	-	unknown	similar to conserved hypothetical protein	5.2
4907.2	5893	lpp2897	3309640	3310404	p	-	unknown	similar to unknown protein	5.2
2297.3	4261	lpp2898	3310516	3310986	p	-	unknown	similar to SsrA-binding protein	3.6
2295.3	4260	lpp2899	3310998	3311462	p	-	unknown	Highly similar to bacterioferritin comigratory protein	5.2

Table XIV

2882.2	4605	lpp2945	3361526	3362212	m	+	unknown	Highly similar to transcriptional regulator ExsB	3.5.2
2167.2	4204	lpp2946	3362302	3363738	p	-	unknown	Highly similar to mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	1.1 6
2166.2	4203	lpp2947	3363966	3365879	p	-	unknown	Highly similar to glucose-inhibited division protein A GidA	1.7
1976.2	4102	lpp2948	3366010	3367884	p	-	unknown	Similar to glucose inhibited division protein B GidB	1.7
1978.1	4103	lpp2949	3367881	3368507	p	-	unknown	Highly similar to chromosome partitioning protein ParA family	3.4
1979.1	4104	lpp2950	3368510	3369280	p	-	unknown	similar to chromosome partitioning protein parB	3.4
122.4	3640	lpp2951	3369294	3370199	p	+	unknown	Similar to hypothetical protein	5.2
121.1	3635	lpp2952	3370307	3370642	p	-	unknown	Similar to transposase (IS5 family)	4.5
119.1	3625	lpp2953	3370963	3371412	m	-	Unknown		6
118.1	3618	lpp2954	3371800	3372387	m	-	unknown		6
116.1	3609	lpp2955	3373298	3373855	m	-	unknown		2.1.1
115.2	3603	lpp2956	3374194	3374700	m	-	unknown	Similar to acetyltransferases	6
114.2	3598	lpp2957	3374783	3374926	m	-	unknown	hypothetical gene	6
2884.1	4606	lpp2958	3375531	3375803	p	-	unknown		1.4
1750.3	3967	lpp2959	3375826	3376695	m	-	cytochrome c oxidase, subunit III		1.4
1752.2	3968	lpp2960	3376854	3377396	m	+	cytochrome c oxidase assembly protein		1.4
1691.3	3928	lpp2961	3377409	3379025	m	-	cytochrome c oxidase, subunit I		1.4
1689.3	3926	lpp2962	3379022	3380227	m	+	cytochrome c oxidase, subunit II		1.4
4542.4	5660	lpp2963	3380309	3381922	m	+	unknown	similar to cytochrome c	1.4
2372.3	4310	lpp2964	3382304	3382657	p	-	Unknown	similar to ferredoxin component of dioxxygenase	1.4
2371.1	4309	lpp2965	3382723	3383751	p	-	unknown	similar to glycosyltransferases	1.1
2369.3	4308	lpp2966	3383810	3384415	p	+	unknown	Similar to transporter, LysE family	1.2
4546.3	5661	lpp2967	3384600	3385652	m	-	unknown		6
3009.2	4691	lpp2968	3386173	3387123	p	+	unknown		6

Table XIV

2579.2	4444	lpp2969	3387424	3387849	p	-	unknown	Similar to conserved hypothetical protein	5.2
2580.2	4445	lpp2970	3387974	3388726	p	-	Ubiquinone/menaquinone biosynthesis methyltransferase		
3008.1	4690	lpp2971	3388734	3389351	p	-	unknown	similar to conserved hypothetical protein	2.5
182.3	4014	lpp2972	3389441	3391090	p	-	unknown	similar to P.aeruginosa probable ubiquinone biosynthesis protein ubiB	5.2
180.1	4001	lpp2973	3391092	3391277	p	+	tatA		2.5
179.1	3994	lpp2974	3391274	3391543	p	-	Putative TatA protein(twin arginine translocation)		1.6
178.1	3986	lpp2975	3391586	3391846	m	-	unknown		1.6
176.1	3973	lpp2976	3392008	3392991	p	-	unknown		6
174.1	3959	lpp2977	3393015	3393884	m	-	unknown	Highly similar to peptide methionine sulfoxide reductase	6
172.1	3946	lpp2978	3394545	3394733	p	-	unknown	similar to hypothetical protein	4.2
2044.2	4134	lpp2979	3394781	3396715	m	-	unknown	similar to copper amine oxidase	5.2
323.2	4813	lpp2980	3397955	3399442	p	-	unknown		2.2
321.3	4804	lpp2981	3399827	3400720	m	-	unknown		6
6277.1	6360	lpp2982	3400988	3401179	p	-	unknown		6
3005.2	4689	lpp2983	3401767	3402270	m	-	unknown	Hypothetical gene	6
5208.1	6042	lpp2984	3402282	3402566	m	-	unknown	Weakly similar to acetyltransferases	2.1.1
1817.2	4011	lpp2985	3403078	3403581	m	-	unknown	Weakly similar to conserved hypothetical protein	5.2
1815.2	4010	lpp2986	3403971	3404498	m	-	unknown		6
2374.2	4312	lpp2987	3404826	3405722	m	-	unknown	Similar to acetyltransferase	2.1.1
2373.2	4311	lpp2988	3406047	3407009	m	+	unknown		6
412.3	5373	lpp2989	3407344	3408537	m	+	unknown	Highly similar to putative lytic murein transglycosylase	1.1
410.1	5358	lpp2990	3408534	3409223	m	-	unknown	similar to ABC transporter permease protein	1.2
409.2	5352	lpp2991	3409216	3410361	m	-	unknown	similar to ATP-binding protein of ABC transporter	1.2
								conserved lipoprotein	1.2

Table XIV

408.3	5345	lpp2992	3410358	3411986	m	+	unknown	Similar to outer membrane efflux protein	1.2
1983.1	4105	lpp2993	3412030	3412860	m	-	apaH	similar to bis(5'-nucleosyl)-tetraphosphatase ApaH	2.3
1986.2	4106	lpp2994	3412853	3414190	m	-		similar to unknown protein	5.2
2800.1	4568	lpp2995	3414227	3414997	m	-	ksgA	similar to dimethyladenosine transferase (16S rRNA dimethylase)	3.6
2799.1	4567	lpp2996	3415333	3415734	p	-	panD	similar to aspartate 1-decarboxylase	2.5
2199.2	4214	lpp2997	3415840	3416565	p	-	tatC	Similar to Sec-independent protein translocase TatC	1.6
2198.1	4213	lpp2998	3416627	3416938	p	-		similar to conserved hypothetical protein	5.2
2197.1	4212	lpp2999	3416976	3417170	m	-			6.
2196.1	4211	lpp3000	3417188	3417901	m	-		Similar to C-terminal part of NAD(P)H-flavin reductase	2.1.1
2195.1	4210	lpp3001	3417901	3419367	m	-	ubiD	Highly similar to 3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases	2.5
2193.4	4209	lpp3002	3419513	3420775	m	-	rho	transcription termination factor Rho	3.5.4
841.3	6483	lpp3003	3421098	3421424	m	-	trxA	Highly similar to thioredoxin	1.4
840.2	6482	lpp3004	3421637	3422371	m	-		Similar to conserved hypothetical protein	5.2
838.3	6480	lpp3005	3422616	3424010	p	-	fumC	fumarate hydratase, class II	2.1.3
2112.2	4167	lpp3006	3424223	3425650	m	+		similar to unknown protein	5.2
1891.2	4056	lpp3007	3425932	3426693	p	-		Similar to hypothetical protein	5.2
4251.2	5466	lpp3008	3426719	3428029	p	-			6
4249.1	5464	lpp3009	3428505	3429689	m	-			6
4248.1	5463	lpp3010	3429757	3430020	m	-		similar to unknown protein	5.2
1081.2	3559	lpp3011	3430495	3431640	p	-			6
1080.2	3558	lpp3012	3431846	3432682	m	-		similar to lipid A biosynthesis lauroyl acyltransferase	2.4
4247.2	5462	lpp3013	3432675	3433523	m	-		similar to acyl transferase	2.4
2353.3	4295	lpp3014	3433682	3434839	p	-	lpxB	Similar to lipid A-disaccharide synthase	1.1

Table XIV

2352.2	4294	lpp3015	3434811	3435842	m	-	lpxD	unknown	Similar to UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	1.1
2351.2	4293	lpp3016	3435858	3436688	m	-	lpxA	unknown	Similar to acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase	1.1 6
3663.1	5090	lpp3017	3436849	3437850	m	-		unknown	Similar to glycosyltransferase	1.1
3664.1	5091	lpp3018	3438064	3439218	m	-		unknown	Similar to methyltransferase	2.1.1
3665.1	5092	lpp3019	3439337	3440257	m	-		unknown	similar to glycosyltransferase	1.1
3666.2	5093	lpp3020	3440254	3441507	m	-		unknown	Highly similar to cystathionine beta-synthase	6
3667.1	5094	lpp3021	3441637	3441903	m	-		unknown		2.2
3669.1	5095	lpp3022	3442481	3443431	p	-	cysK	unknown	Some similarity with eukaryotic proteins	6
3670.2	5096	lpp3023	3443526	3444569	m	-		unknown	Highly similar to integration host factor, beta subunit	6
3671.2	5097	lpp3024	3445155	3445880	p	-		unknown		5.2
3415.2	4925	lpp3025	3446065	3446601	p	-		unknown		4.4
3416.1	4926	lpp3026	3446854	3447165	p	-	himD	unknown	Similar to protease	2.3
3417.1	4927	lpp3027	3447181	3447747	m	-	dcd	deoxycytidine triphosphate deaminase	Putative transmembrane protein, similar to hypothetical membrane-bound serine protease	2.2
453.3	5650	lpp3028	3447986	3448741	m	-		unknown	Conserved hypothetical protein	5.2
454.1	5658	lpp3029	3448785	3450290	m	-		unknown	Similar to major outer membrane protein precursor	1.1
457.2	5673	lpp3030	3450499	3452091	m	+		unknown		1.1
2053.2	4137	lpp3031	3452394	3453365	m	+		unknown	Similar to sodium-type flagellar protein MotY	1.5
3418.2	4928	lpp3032	3453438	3454307	m	+		major outer membrane protein	Similar to dihydroorotase, homodimeric type	2.3
5898.4	6296	lpp3033	3454473	3455342	m	+		major outer membrane protein precursor		
523.2	6050	lpp3034	3455653	3456537	m	+		unknown		
524.2	6053	lpp3035	3456607	3457644	p	-	pyrC	unknown		

Table XIV

526.2	6061	lpp3036	3457628	3458251	p	-	rnsT	ribonuclease T	2.3
528.2	6067	lpp3037	3458377	3458982	m	-	ahpC	alkyl hydroperoxide reductase	4.2
529.2	6071	lpp3038	3459035	3459382	m	-	grlA	glutaredoxin-like protein	4.2
3609.1	5053	lpp3039	3459683	3460261	p	-	sodB	superoxide dismutase, iron	4.2
3610.1	5054	lpp3040	3460321	3461490	p	-	argD	Similar to ornithine/acetylornithine aminotransferase	2.2
3611.2	5055	lpp3041	3461619	3462386	m	-		Similar to conserved hypothetical protein	5.2
3612.2	5056	lpp3042	3462542	3463324	m	-		Similar to glycerophosphoryl diester phosphodiesterase (ATA start codon)	2.4
3613.4	5057	lpp3043	3463576	3465246	p	-		Similar to NAD-linked malate dehydrogenase (malic enzyme)	2.1.1
5905.3	6303	lpp3044	3465476	3466444	p	-		Similar to putative translation initiation protein	3.7.3
6273.1	6359	lpp3045	3466542	3466625	p	-		hypothetical gene	5.2
2828.5	4584	lpp3046	3466618	3467469	m	-	psd	Phosphatidylserine decarboxylase	2.4
2827.3	4583	lpp3047	3467562	3470177	m	-		unknown	6
2826.1	4582	lpp3048	3470440	3471969	m	-		unknown	6
2119.2	4169	lpp3049	3472423	3474084	m	+		unknown	2.2
909.2	6530	lpp3050	3474336	3475190	p	-		unknown	5.2
910.4	6531	lpp3051	3475297	3477552	m	-	parC	DNA topoisomerase IV, A subunit	3.4
2824.1	4581	lpp3052	3478181	3478603	m	-	atpC	Highly similar to H ⁺ -transporting ATP synthase epsilon chain	1.4
1556.2	3839	lpp3053	3478615	3479991	m	-	atpD	Highly similar to H ⁺ -transporting ATP synthase beta chain	1.4
1555.2	3838	lpp3054	3480004	3480870	m	-	atpG	Highly similar to H ⁺ -transporting ATP synthase chain gamma	1.4
1552.3	3837	lpp3055	3480960	3482513	m	-	atpA	Highly similar to H ⁺ -transporting ATP synthase chain alpha	1.4

Table XIV

2140.2	4185	lpp3056	3482531	3483073	m	-	atpH	unknown	Highly similar to H ⁺ -transporting ATP synthase chain delta	1.4
2138.2	4183	lpp3057	3483075	3483545	m	-	atpF	unknown	Highly similar to H ⁺ -transporting ATP synthase chain b	1.4
2137.1	4182	lpp3058	3483597	3483872	m	-	atpE	unknown	Highly similar to H ⁺ -transporting ATP synthase chain c	1.4
2136.1	4181	lpp3059	3483913	3484749	m	-	atpB	unknown	Highly similar to H ⁺ -transporting ATP synthase chain a	1.4
2135.1	4180	lpp3060	3484742	3485137	m	+	atpI	unknown	Similar to ATP synthase subunit i	1.4
2133.1	4179	lpp3061	3485291	3485536	p	-		Unknown		6.
2132.2	4178	lpp3062	3485606	3486193	m	+		unknown	Similar to lipoproteins	1.2
2130.1	4177	lpp3063	3486195	3486767	m	+		unknown	similar to lipoproteins	1.2
2129.1	4175	lpp3064	3486771	3487370	m	-		unknown	similar to phosphoheptose isomerase	2.1.1
2127.2	4174	lpp3065	3487397	3487753	m	-		unknown	similar to conserved hypothetical protein	5.2
2822.1	4580	lpp3066	3487775	3489586	m	+		unknown	conserved hypothetical protein, putative lipoprotein	5.2
2820.1	4579	lpp3067	3489626	3490477	p	-		unknown	conserved hypothetical protein, putative methyltransferase	5.2
2818.1	4577	lpp3068	3490607	3491674	p	-		unknown	similar to alkane monooxygenase	2.1.1
2816.2	4576	lpp3069	3491725	3493890	m	+		unknown	Similar to sulfate permease and related transporters (MFS superfamily) with a C-terminal cAMP binding motif.	1.2
2815.2	4575	lpp3070	3494454	3496214	p	-		unknown		6
2565.4	4436	lpp3071	3496419	3497219	p	-		unknown	Similar to eukaryotic zinc metalloproteinase	2.2
1176.5	3616	lpp3072	3497216	3499054	m	-		unknown		6
1174.2	3615	lpp3073	3499350	3500690	m	-		unknown	Similar to GTPase for tRNA modification trmE	3.6
5040.2	5970	lpp3074	3500691	3502361	m	+		unknown	putative inner membrane protein	5.2

Table XIV

5039.2	5969	lpp3075	3502371	3502616	m	-	unknown	Similar to conserved hypothetical protein	5.2
5038.1	5968	lpp3076	3502583	3502927	m	-	unknown	similar to ribonuclease P protein component (RNase P)	3.6
5037.2	5967	lpp3077	3502928	3503062	m	-	rpmH	50S ribosomal protein L34	3.7.1
739.5	6715	plpp0001	66	941	m	-	parB	highly similar to partition protein parB	3.4
4947.2	6684	plpp0002	1297	2505	p	-	unknown	Highly similar to partition protein SopA/ParA	3.4
4945.2	6683	plpp0003	2507	3514	p	-	unknown	similar to hypothetical replication protein RepB	3.1
5078.2	6685	plpp0004	3552	4841	p	-	unknown	similar to hypothetical replicative protein RepA	3.1
5081.5	6687	plpp0005	4992	5558	p	+	unknown	similar to unknown proteins	5.2
5080.6	6686	plpp0006	5591	7045	p	-	unknown	similar to major facilitator superfamily (MFS) transporter	1.2
5106.3	6688	plpp0007	7047	8069	m	-	unknown		6
6227.1	6702	plpp0008	8091	8285	m	-	Unknown		6.
5147.1	6691	plpp0009	8469	9731	p	-	unknown		6
3500.3	6674	plpp0010	9688	10866	p	-	Unknown	similar to unknown protein	5.2
3499.1	6673	plpp0011	11016	11267	p	-	Unknown	similar to molybdopterin converting factor 2 (subunit 1)	2.5
1226.2	6597	plpp0012	11272	12294	p	-	Unknown	similar to molybdenum cofactor synthesis protein 3	2.5
1225.2	6596	plpp0013	12291	13352	p	-	unknown	Weakly similar to conserved hypothetical proteins	5.2
2275.4	6632	plpp0014	13345	14379	p	-	Unknown		5.2
6229.1	6703	plpp0015	14492	14677	p	-	Unknown		6.
6230.1	6704	plpp0016	14712	14972	p	-	unknown	Weakly similar to carbon storage regulator CsrA	3.5.2
1171.4	6594	plpp0017	14997	15743	p	+	unknown	Similar to E.coli TraT complement resistance protein	4.5
1172.2	6595	plpp0018	15837	16181	p	-	unknown		6
3498.1	6672	plpp0019	16301	16657	p	+	unknown		6
6231.3	6705	plpp0020	16712	17758	p	-	unknown	similar to transposase	4.5
6224.3	6701	plpp0021	17755	18549	p	-	unknown	similar to plasmid DNA replication protein	3.1

Table XIV

2659.3	6638	plpp0022	18713	19036	p	+	unknown	similar to fimbrial protein precursor (PilIn)	1.8
2660.1	6639	plpp0023	19026	19316	p	-	unknown	weakly similar to conjugative transfer protein TraL	4.5
2661.2	6640	plpp0024	19321	19878	p	-	unknown	Weakly similar to conjugative transfer protein TraE	4.5
2662.2	6641	plpp0025	19875	20594	p	+	unknown	Weakly similar to conjugative transfer protein TraK	4.5
485.3	6681	plpp0026	20609	22063	p	+	unknown	weakly similar to conjugative transfer protein TraB	4.5
486.2	6682	plpp0027	22056	22283	p	-	unknown	hypothetical gene	6
254.2	6633	plpp0028	22313	24889	p	-	unknown	weakly similar to conjugative transfer protein TraC	4.5
255.1	6634	plpp0029	24879	25214	p	+	unknown	Weakly similar to TrbI protein	4.5
256.1	6635	plpp0030	25211	25837	p	-	unknown	weakly similar to conjugative transfer protein TraW	4.5
258.2	6637	plpp0031	25849	26844	p	+	unknown	similar to conjugative transfer protein TraU	4.5
2006.2	6616	plpp0032	26861	27523	p	+	unknown	Weakly similar to conjugative transfer protein TrbC	4.5
1344.4	6603	plpp0033	27516	29315	p	+	Unknown	Similar to putative conjugative transfer protein TraN	4.5
1342.3	6602	plpp0034	29312	30100	p	+	unknown	Similar to putative conjugative transfer protein TraF	4.5
2051.2	6617	plpp0035	30097	30594	p	+	unknown	Weakly similar to putative conjugative transfer protein TrbB	4.5
1299.3	6601	plpp0036	30612	31988	p	+	unknown	Similar to conjugative transfer protein TraH	4.5
567.6	6696	plpp0037	31985	34744	p	-	unknown	similar to sex pilus assembly and mating pair protein TraG	4.5
2212.4	6626	plpp0038	34823	36826	p	+	unknown	Highly similar to conjugative transfer protein TraD	4.5
1599.5	6610	plpp0039	36848	42715	p	-	unknown	similar to conjugative transfer protein TraI	4.5
2665.1	6642	plpp0040	42895	43176	p	-	unknown		6
2666.1	6643	plpp0041	43309	43629	m	-	unknown		6
2667.2	6644	plpp0042	43620	44069	m	-	Unknown		6
717.3	6713	plpp0043	44445	44891	p	-	unknown		6

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716.1	6712	plpp0044	44933	45136	p	-	unknown	6
715.1	6711	plpp0045	45305	45622	p	-	unknown	6
713.2	6710	plpp0046	45695	46039	p	+	unknown	6
5844.1	6697	plpp0047	46327	46731	m	-	unknown	3.2
4483.2	6679	plpp0048	46854	47477	m	-	unknown	6
4482.1	6678	plpp0049	47722	48621	p	-	unknown	4.4
4481.1	6677	plpp0050	48703	49233	m	-	unknown	5.2
3632.3	6676	plpp0051	49324	52371	m	-	Unknown	4.5
2244.2	6627	plpp0052	52521	53126	p	-	unknown	3.3
2245.2	6628	plpp0053	53129	54202	p	-	unknown	5.2
2247.7	6629	plpp0054	54192	55985	p	-	unknown	1.2
783.2	6721	plpp0055	56024	56380	m	-	unknown	5.2
785.4	6722	plpp0056	56410	57264	m	+	unknown	6
5846.2	6698	plpp0057	57242	57415	m	-	Unknown	6.
3631.4	6675	plpp0058	57472	57702	m	-	unknown	6
6016.1	6700	plpp0059	57783	58091	m	-	unknown	6
6015.1	6699	plpp0060	58262	58546	p	-	unknown	6
5113.3	6689	plpp0061	58548	58988	p	-	unknown	6
5114.3	6690	plpp0062	59104	59916	p	-	unknown	6
3138.2	6659	plpp0063	59972	60844	p	-	unknown	6
3137.1	6658	plpp0064	60896	61381	p	+	Unknown	6.
3136.1	6657	plpp0065	61462	61791	p	-	unknown	5.2
799.3	6725	plpp0066	62005	63480	p	-	unknown	1.2
798.2	6724	plpp0067	63461	65260	p	+	unknown	1.2

similar to putative anti restriction protein KlcA

Similar to abortive infection bacteriophage resistance protein

Similar to eukaryotic hypersensitive-induced response protein

Similar to transposase (Tn3 family)

Similar to resolvase TnpR

Similar to conserved hypothetical protein

Similar to ABC transporter (ATP-binding protein)

similar to unknown proteins

hypothetical gene

Weakly similar to conserved hypothetical protein

Similar to ATPase components of ABC transporters

Similar to multidrug resistance ABC transporter ATP-binding protein

Table XIV

796.2	6723	plpp0068	65253	66035	p	-	unknown	Weakly similar to Legionella longbeachae spectinomycin 3 adenylyltransferase	5.1
2087.2	6618	plpp0069	66036	66995	p	-	unknown	N-terminal part similar to conserved hypothetical protein	5.2
2180.2	6625	plpp0070	66992	68476	p	-	unknown	Fusion of three acetyltransferase	2.1.1
3135.1	6656	plpp0071	68473	68685	p	-	unknown	Similar to conserved hypothetical protein	5.2
3134.1	6655	plpp0072	68678	69250	p	-	unknown	Similar to hypothetical protein	5.2
1762.2	6612	plpp0073	69327	70271	p	-	unknown	Weakly similar to MerR family transcriptional regulators	3.5.2
1761.4	6611	plpp0074	70485	73598	p	-	unknown	penicillin binding protein domain	1.1
1575.2	6609	plpp0075	73929	74351	p	-	unknown	Similar to transcriptional regulators	3.5.2
3346.2	6660	plpp0076	74354	76276	p	-	unknown	similar to penicillin-binding protein 2 (FtsI)	1.1
3347.1	6661	plpp0077	76344	77144	p	+	unknown	Similar to beta-lactamase	4.2
3348.3	6662	plpp0078	77148	78728	p	+	Unknown	hypothetical polysaccharide deacetylase-related, fusion protein	2.1.1
3349.3	6663	plpp0079	78732	79628	p	-	unknown	Similar to conserved hypothetical protein	5.2
3350.3	6664	plpp0080	79771	80133	p	-	unknown	Similar to unknown protein	5.2
3351.3	6665	plpp0081	80153	81325	p	-	unknown	Similar to dihydrofolate reductase and methyltransferase	2.5
3352.1	6666	plpp0082	81354	81824	m	-	unknown	Similar to acetyltransferase, GNAT family	2.1.1
3353.1	6667	plpp0083	81973	83481	p	-	unknown	Similar to hypothetical protein	5.2
3354.1	6668	plpp0084	83532	84107	p	-	unknown	Similar to pyridoxamine 5 - phosphate oxidase	2.5
960.2	6732	plpp0085	84116	84427	p	-	unknown	similar to unknown protein	5.2
959.2	6731	plpp0086	84483	84665	p	-	unknown	hypothetical gene	6
957.2	6730	plpp0087	84759	85634	m	-	unknown	Weakly similar to alpha/beta hydrolase fold family protein	2.1.1
956.2	6729	plpp0088	85692	86453	m	-	unknown	Similar to transcriptional regulator	3.5.2

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3355.2	6669	plpp0089	86666	86953	m	-	unknown	Weakly similar to stability protein StbE	4.5
3356.2	6670	plpp0090	86943	87194	m	-	unknown	Weakly similar to stability protein StbD	4.5
3357.2	6671	plpp0091	87443	87910	m	-	unknown		6
5154.2	6695	plpp0092	88529	89350	m	-	unknown	Highly similar to spectinomycin 3 adenylyltransferase	4.2
5153.1	6694	plpp0093	89334	89771	m	-	unknown	Highly similar to Legionella longbeachae unknown protein	5.1
2573.3	6636	plpp0094	89758	90336	m	-	unknown	Highly similar to Legionella longbeachae unknown protein	5.1
2881.3	6650	plpp0095	90624	91529	m	-	unknown		6
2879.4	6649	plpp0096	91618	92943	m	-	unknown	similar to unknown protein	5.2
2878.2	6648	plpp0097	93135	93827	p	-	IrpR unknown	Highly similar to Legionella longbeachae putative transcriptional regulatory protein	3.5.2
1362.3	6604	plpp0098	94067	95890	p	-	unknown	Highly similar to Legionella longbeachae unknown protein, ankyrin repeat containing protein	5.1
1364.2	6605	plpp0099	95894	97498	m	+	IskS unknown	Highly similar to L. longbeachae sensor histidine kinase protein	1.3
2877.2	6647	plpp0100	97597	98253	m	-	unknown	Similar to hypothetical protein	5.2
2175.3	6622	plpp0101	98341	98559	m	-	unknown		6
2174.1	6621	plpp0102	98563	98859	m	-	unknown	conserved hypothetical protein	5.2
1078.2	6593	plpp0103	99016	99993	p	-	unknown		6
1077.1	6592	plpp0104	100101	100793	p	-	unknown	Similar to hypothetical transcriptional regulator	3.5.2
1076.3	6591	plpp0105	100869	101237	p	-	unknown	conserved hypothetical protein	5.2
2173.2	6620	plpp0106	101240	101668	p	-	unknown	similar to hypothetical protein	5.2
2172.2	6619	plpp0107	101692	102153	p	-	unknown	Weakly similar to probable transcriptional regulator	3.5.2
2874.1	6646	plpp0108	102176	102919	p	-	unknown	Weakly similar to DNA alkylation repair enzyme	3.2
2873.1	6645	plpp0109	102950	103921	m	-	unknown	Similar to hypothetical protein	5.2
761.2	6716	plpp0110	103938	104891	m	-	unknown	C-terminal part similar to acetyltransferase	2.1.1

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762.2	6717	plpp0111	105014	105661	p	+	unknown	weakly similar to lysE family transporter protein	1.2
764.1	6718	plpp0112	105738	106253	p	-	unknown	similar to acetyltransferase protein	2.1.1
765.1	6719	plpp0113	106325	107044	m	-	unknown	Similar to N-terminal part of hypothetical protein	5.2
766.4	6720	plpp0114	107216	108649	m	-	unknown	similar to esterase	4.1
886.4	6728	plpp0115	108721	109491	m	-	unknown	similar to shikimate kinase (AroK)	2.2
885.3	6727	plpp0116	109545	111149	p	-	unknown	similar to aminoglycoside 3 - phosphotransferase	4.2
884.3	6726	plpp0117	111146	112111	p	-	unknown		6
4549.2	6680	plpp0118	112324	113640	p	-	unknown	Putative adenine-specific DNA methylase	3.2
1237.2	6600	plpp0119	113656	114093	p	-	unknown	Weakly similar to acetyltransferase	2.1.1
1236.2	6599	plpp0120	114212	115009	m	-	unknown		5.1
1235.3	6598	plpp0121	115070	115798	m	-	unknown	Weakly similar to acetyltransferase	2.1.1
5152.1	6693	plpp0122	115804	116190	m	-	unknown	Similar to unknown protein	5.2
5151.1	6692	plpp0123	116238	117131	m	-	unknown	similar to unknown protein	5.2
1848.5	6613	plpp0124	117144	118394	m	-	unknown	bifunctional protein, similar to acetyl transferase and to methyl transferase	4.6
1849.4	6614	plpp0125	118391	118855	m	-	unknown	similar to acetyltransferase, GNAT family	2.1.1
1852.2	6615	plpp0126	118878	119234	m	-	unknown	Similar to conserved hypothetical protein	5.2
1522.2	6606	plpp0127	119231	120406	m	-	unknown	similar to acetyltransferase (C-terminal part)	4.6
1523.2	6607	plpp0128	120457	120729	m	-	unknown		6
1524.3	6608	plpp0129	120790	121833	m	-	unknown	Some similarity with transcriptional regulator, MerR family	3.5.2
2258.2	6630	plpp0130	122086	123333	m	-	unknown		6
2260.2	6631	plpp0131	123311	123985	m	-	unknown	Similar to alanyl tRNA synthetase	3.7.2
3030.2	6651	plpp0132	123989	124480	m	-	unknown	Similar to hypothetical protein	5.2
3031.2	6652	plpp0133	124497	124919	m	-	unknown		6

Table XIV

3035.2	6653	plpp0134	125023	125598	p	-	unknown	Weakly similar to transcriptional regulator	3.5.2
659.2	6707	plpp0135	125603	126556	m	-	unknown	Similar to conserved hypothetical protein	5.2
660.1	6708	plpp0136	126553	127119	m	-	unknown	Weakly similar to acetyltransferase	2.1.1
661.3	6709	plpp0137	127106	128239	m	-	unknown	C-terminal part similar to acetyltransferase	2.1.1
3036.2	6654	plpp0138	128246	128788	m	-	unknown	Weakly similar to DNA topology modulation protein	3.4
2176.3	6623	plpp0139	128871	129329	m	-	unknown	weakly similar to regulatory protein recX	3.3
2177.2	6624	plpp0140	129429	130013	p	-	unknown	Similar to integrase proteins	4.5
737.2	6714	plpp0141	130347	131369	m	-	unknown	similar to ATP-dependent DNA helicase RecG(C-terminal part)	3.3
6429.1	6706	plpp0141a	131326	131850	m	-	unknown	Similar to N-terminal part of ATP-dependent DNA helicase recG	3.3

Table XVI:

ORF	SEQ ID	EMBL NAME	Posit°1	Posit°2	Sens	SignalP	Name of the gene	Product of the gene	Note	Class
1955.1	6810	lp10904	1015112	1016491	m	-		unknown		6
2100.1	6811	lp11006	1140978	1141112	p	-		unknown	hypothetical gene	6
2110.1	6812	lp11015	1147633	1149258	m	-		unknown	Some similarity with RNA-directed DNA polymerase	3.1
2134.1	6813	lp11034	1164732	1165319	m	-		unknown		6
2135.1	6814	lp11035	1165316	1165729	m	+		unknown	Similar to PilL protein	1.8
2136.1	6815	lp11036	1165738	1165938	m	-		unknown	Similar to carbon storage regulator	3.5.2
2137.1	6816	lp11037	1165932	1166450	m	-		unknown	Similar to Legionella LvrB protein	5.1
2139.1	6817	lp11039	1167370	1167624	p	-		unknown	Similar to phage repressor	4.4
2141.1	6818	lp11041	1168453	1168914	m	+		unknown	Similar to putative lipoprotein	5.1
2142.2	6819	lp11042	1169480	1170091	m	-		unknown	Similar to conserved hypothetical protein	5.2
2144.1	6820	lp11043b	1170400	1170588	m			unknown	Similar to C-terminal part of arginine-binding periplasmic protein	1.2
2145.1	6821	lp11043a	1170581	1170910	m			unknown	Similar to central part of arginine-binding periplasmic protein	1.2
2151.1	6822	lp11047	1176999	1177199	m	+		unknown	Hypothetical protein	6
2152.2	6823	lp11048	1177363	1177659	p	-		unknown	Weakly similar to transcriptional regulator	3.5.2
2155.1	6824	lp11050	1180093	1180326	m			Unknown		6
2157.1	6825	lp11051	1180809	1180973	p	-		unknown	Hypothetical protein	6
2168.1	6826	lp11058	1186757	1186903	m	-		unknown	Similar to C-terminal part of unknown protein	5.1
2170.1	6827	lp11059	1187369	1188397	p	-		unknown	Similar to EnhC protein, contains 7 sel-1 domains	4.6
2180.1	6828	lp11067	1194223	1195173	m			unknown		6

2181.1	6829	lpl1068	1195308	1198694	m	-	unknown	Some similarity with helicase proteins	3.2
2182.1	6830	lpl1069	1198678	1200126	m	-	unknown		6
2184.1	6831	lpl1070	1200113	1200817	m	-	unknown	Weakly similar to chemotaxis motB protein	1.5
2186.2	6832	lpl1071	1200795	1202768	m		Unknown	Hypothetical protein	6
2189.1	6833	lpl1073	1203936	1205711	p	-	unknown	Similar to conserved hypothetical protein	5.2
2192.1	6834	lpl1075	1207092	1207256	p		unknown	Hypothetical protein	6
2194.1	6835	lpl1076	1207510	1208286	p	-	unknown	Similar to hypothetical protein	5.2
2195.1	6836	lpl1077	1208304	1208747	m		Unknown	hypothetical gene	6
2198.1	6837	lpl1080	1209864	1210679	m	-	unknown		6
2199.1	6838	lpl1081	1210788	1211342	p	-	unknown		6
2200.1	6839	lpl1082	1211557	1211928	p	-	unknown		6
2201.1	6840	lpl1083	1211925	1212284	p	-	unknown	Similar to conserved hypothetical protein	5.2
2202.1	6841	lpl1084	1212352	1212606	p	-	unknown	Similar to DNA-damage-inducible protein J	3.2
2203.1	6842	lpl1085	1212983	1214224	m	-	unknown	Similar to phage-related integrase proteins	4.4
2205.1	6843	lpl1086	1214553	1214804	m	-	unknown		6
2206.1	6844	lpl1087	1214933	1216825	m	-	unknown	Similar to conserved hypothetical protein	5.2
2207.1	6845	lpl1088	1216892	1217056	m	-	unknown	Hypothetical protein	6
2208.1	6846	lpl1089	1217691	1218077	p		Unknown		6
2209.1	6847	lpl1090	1218170	1218307	p	-	unknown	Hypothetical protein	6
2210.1	6848	lpl1091	1218451	1218768	m	-	unknown	Weakly similar to DNA-binding protein	3.5.2
2211.1	6849	lpl1092	1219050	1219331	p	-	unknown	Similar to plasmid maintenance system killer protein	4.5

2213.1	6850	lpl1093	1219338	1219661	p	-	unknown	Similar to plasmid maintenance system antidote protein	4.5
2224.1	6851	lpl1101	1225340	1226203	m	-	unknown		6
2238.1	6852	lpl1110	1235461	1235754	p	-	unknown	Similar to transposase	4.5
4011.1	7007	lpl1113	1237989	1238123	m	-	unknown	hypothetical protein	6
4007.1	7006	lpl1116	1239963	1240346	m	-	unknown		6
3995.1	7005	lpl1125	1251579	1251812	m	-	unknown		6
3987.1	7004	lpl1132	1261359	1263053	p	+	unknown	Similar to glutathione-regulated potassium-efflux system protein kefC (K(+)/H(+)) antiporter	1.2
3976.1	7003	lpl1138	1269104	1270132	m	-	unknown	Similar to transposase, IS630 family	4.5
3949.1	7002	lpl1158	1291134	1292444	m	-	unknown	Some similarity with eukaryotic proteins	6
3937.1	7001	lpl1165	1301149	1301286	p	-	unknown	Hypothetical protein	6
4229.2	7027	lpl1393	1555031	1555522	m	-	unknown		6
175.1	6802	lpl0132	157452	157604	m	-	unknown	hypothetical, similar to hypothetical proteins	6
4203.1	7026	lpl1412	1575836	1576864	p	-	unknown	Similar to transposase, IS630 family	4.5
4197.1	7025	lpl1416	1581011	1582300	m	-	unknown	Similar to major facilitator family (MFS) transporter	1.2
4196.1	7024	lpl1417	1582309	1583310	m	-	unknown	Similar to conserved hypothetical protein	5.2
4189.2	7023	lpl1424	1590828	1592246	p	-	unknown	Similar to transposase	4.5
898.1	7057	lpl1425	1592331	1592816	p	-	unknown	Similar to transposase (truncated)	4.5
761.1	7056	lpl1536	1711241	1711603	m	-	unknown		6
760.1	7055	lpl1537	1711726	1711977	m	-	unknown	Weakly similar to mitomycin resistance protein	4.1
711.1	7054	lpl1574	1755441	1755842	m	-	unknown	Hypothetical protein	6
709.1	7053	lpl1575	1755944	1756645	m	-	unknown	Similar to replication protein	3.1
707.1	7052	lpl1577	1757623	1757916	m	-	unknown	Similar to transposase	4.5

705.1	7051	lpl1578	1757963	1758193	m		unknown	Similar to N-terminal part of replication protein	3.1
703.1	7050	lpl1579	1758826	1760220	p	-	unknown	Similar to other proteins	6
159.1	6799	lpl0143	175902	177617	p	-	unknown		6
700.1	7049	lpl1580	1760423	1761040	m	-	unknown		6
699.1	7048	lpl1581	1761052	1762173	m	-	unknown	Similar to part of conjugal transfer protein traA	4.5
697.1	7047	lpl1582	1762266	1762577	m	-	unknown	Similar to transposase	4.5
694.1	7046	lpl1584	1763137	1763430	m	-	unknown	Similar to transposase	4.5
692.1	7045	lpl1585	1763491	1764834	m		unknown	Similar to N-terminal part of conjugal transfer protein TraA	4.5
690.1	7044	lpl1586	1765077	1765298	p	-	unknown	Hypothetical protein	6
689.1	7043	lpl1587	1765353	1765601	p	-	unknown	Similar to hypothetical protein	5.2
688.1	7042	lpl1588	1765591	1765848	p	-	unknown	Weakly similar to stability protein StbE	4.5
157.1	6798	lpl0144	177672	179090	m	-	unknown	Similar to hypothetical protein	5.2
156.1	6797	lpl0145	179293	180546	p	-	unknown	Similar to cytosine-specific DNA methylase	3.2
154.1	6796	lpl0146	180543	180968	p	-	unknown	Similar to DNA mismatch repair endonuclease	3.2
148.1	6794	lpl0150	183077	183280	p	-	lvrC	similar to carbon storage regulator gene csrA	5.1
566.1	7041	lpl1676	1869326	1869454	m	-	unknown	Hypothetical protein	6
564.1	7040	lpl1678	1870005	1870523	p	-	unknown		6
562.1	7039	lpl1679	1871002	1871832	m	-	unknown		6
561.1	7038	lpl1680	1872034	1873806	p	-	unknown		6
560.1	7037	lpl1681	1873869	1874516	p	-	unknown	Ankyrin repeat protein	4.6
127.1	6778	lpl0164	195255	195590	p	+	unknown		6
126.1	6777	lpl0165	195737	196612	m	-	unknown	Similar to transposase	4.5
125.1	6772	lpl0166	196771	196944	m	-	unknown	Hypothetical protein	6
124.1	6771	lpl0167	197056	197223	p	+	unknown	Hypothetical protein	6

442.1	7036	lpl1768	1971829	1972026	m	+	Unknown	6
117.1	6762	lpl0171	201954	202217	p	-	some similarity with TraD protein	4.5
116.1	6761	lpl0172	202239	202805	p	-		6
115.1	6760	lpl0173	202924	204147	p	-		6
113.1	6758	lpl0174	204158	204652	p	-		6
112.1	6757	lpl0175	204671	205426	p	-	Similar to conserved hypothetical protein	5.2
111.1	6756	lpl0176	205401	206120	m	-	Similar to other proteins	5.2
110.1	6754	lpl0177	206286	206567	p	-		6
322.1	6941	lpl1857	2078673	2078882	m	-	Hypothetical protein	6
106.1	6752	lpl0180	208124	209491	m	-	Similar to predicted ATPase	5.2
105.1	6749	lpl0181	210028	210912	p	-	Similar to predicted Rossmann fold nucleotide-binding protein involved in DNA uptake	1.2
293.1	6924	lpl1879	2104753	2105166	m	-	similar to type IV pilin PilA	1.8
103.1	6740	lpl0182	210914	211552	p	-		6
102.1	6738	lpl0183	211654	211914	p	-	Similar to hypothetical protein	5.2
273.2	6907	lpl1893	2121129	2122547	p	-	Similar to transposase	4.5
1048.1	6747	lpl1894	2122544	2123488	p	-	Similar to transposase	4.5
1047.1	6746	lpl1895	2124195	2125265	m	-	Putative carbonic anhydrase	4.7
1045.1	6745	lpl1896	2125661	2126002	p	-		6
1043.1	6744	lpl1897	2126564	2126761	m	-	Hypothetical protein	6
1041.1	6743	lpl1899	2128985	2131282	m	-	Some similarity with hypothetical protein	5.2
1040.1	6742	lpl1900	2131700	2132722	m	-		6
1038.1	6741	lpl1901	2132987	2133136	p	-	Hypothetical protein	6
4188.1	7022	lpl0185	213723	214016	p	-	Similar to transposase	4.5
1020.1	6739	lpl1915	2147637	2150381	p	-	Some similarity with eukaryotic proteins	5.2
4185.1	7021	lpl0187	214968	217403	p	-	Similar to C-terminal part of type I restriction enzyme	3.2

1003.1	6737	lpl1926	2164000	2164812	p	-	unknown	Weakly similar to putative transcriptional regulator	3.5.2
1002.1	6736	lpl1927	2164842	2165246	m	-	unknown		6
1001.1	6735	lpl1928	2165432	2166199	p	-	unknown		6
997.1	7060	lpl1931	2169048	2170490	p	-	unknown	Some similarity with eukaryotic proteins	5.2
995.2	7059	lpl1933	2171360	2172388	p	-	unknown	Similar to transposase	4.5
4237.1	7029	lpl1934	2172470	2172721	p	-	unknown		6
4182.1	7020	lpl0188	217615	218598	m		unknown	Similar to C-terminal part of predicted nuclease	5.2
4248.1	7030	lpl1942	2179995	2180972	p	-	unknown	Similar to major outer membrane protein momp	1.1
4250.1	7031	lpl1943	2181017	2182399	p	-	unknown	Similar to capsular polysaccharide biosynthesis protein	1.1
4251.1	7032	lpl1944	2182621	2183325	p	-	unknown	Similar to transcriptional regulator	3.5.2
4252.1	7033	lpl1945	2183318	2184877	p	-	unknown	Similar to methionyl-tRNA synthetase	3.7.2
4253.1	7034	lpl1946	2184855	2186192	p	-	unknown	Similar to siderophore biosynthesis protein lucD	2.5
4254.1	7035	lpl1947	2186176	2186526	p	-	unknown	Some similarity with hypothetical protein	5.2
4181.1	7019	lpl0189	218758	220989	p	-	unknown	Some similarity with SidC	5.1
4236.2	7028	lpl1965	2207266	2208294	p	-	unknown	Similar to transposase, IS630 family	4.5
4177.1	7018	lpl0190	221031	221240	m	-	Unknown		6
4175.1	7017	lpl0191	221304	221948	m	-	unknown		6
4174.1	7016	lpl0192	222102	223523	p	-	unknown	Similar to transposase	4.5
4173.1	7015	lpl0193	223610	224104	m		unknown	Similar to predicted nuclease, truncated	5.2
4172.1	7014	lpl0194	224432	225391	p	-	unknown	Similar to virulence protein	5.2
4171.2	7013	lpl0195	225848	227266	p	-	unknown	Similar to transposase	4.5

4170.1	7012	lpl0196	227299	228132	m	-	unknown	Similar to transposase and inactivated derivatives	4.5
899.2	7058	lpl2032	2276023	2277441	p	-	unknown	Similar to transposase	4.5
3162.1	6940	lpl2033	2277621	2278655	m	-	unknown	Similar to transposase	4.5
3161.1	6939	lpl2034	2278869	2279909	m	-	unknown	Similar to threonine dehydrogenase	2.2
3160.1	6938	lpl2035	2280074	2280520	m	-	unknown	Similar to conserved hypothetical protein	5.2
3158.1	6937	lpl2036	2280636	2281013	m	-	unknown	Similar to putative DNA-3-methyladenine glycosylase II	3.2
4169.1	7011	lpl0197	228170	228463	p	-	unknown	Similar to transposase	4.5
3156.1	6936	lpl2037	2282022	2283050	p	-	unknown		6
3155.1	6935	lpl2038	2283257	2283496	m	-	unknown	Hypothetical protein	6
3151.1	6934	lpl2042	2286768	2286950	p	-	unknown	Hypothetical protein	6
2241.1	6853	lpl0199	229638	230066	p	-	unknown	Similar to hypothetical protein	5.2
3140.1	6933	lpl2049	2297022	2298080	p	-	unknown		6
2242.1	6854	lpl0200	230056	231003	p	-	unknown	Similar to hypothetical protein	5.2
2244.1	6855	lpl0201	231474	231704	p	-	Unknown	Tral gene fragment	4.5
2245.1	6856	lpl0202	231520	231810	p	-	Unknown	Tral gene fragment	4.5
2246.1	6857	lpl0203	231882	232007	p	-	Unknown	Tral gene fragment	4.5
2247.1	6858	lpl0204	232253	232501	m	-	unknown	Hypothetical protein	6
2248.1	6859	lpl0205	232524	232730	m	-	unknown	Similar to transposase, truncated	4.5
2253.1	6860	lpl0207	234172	235023	p	-	unknown	Similar to conserved hypothetical protein	5.2
1105.2	6755	lpl0019	23436	24410	m	-	unknown		6
2259.1	6861	lpl0211	237456	238250	p	-	unknown	Similar to conserved hypothetical protein	5.2
3066.1	6932	lpl2098	2378077	2378541	m	-	unknown	Weakly similar to transcriptional regulator, LuxR family	3.5.2
3065.1	6931	lpl2099	2378599	2378952	p	-	unknown		6
3064.1	6930	lpl2100	2379202	2380512	p	-	unknown		6
2260.1	6862	lpl0212	238252	239340	p	-	unknown	Similar to putative aminotransferase	2.2

3057.1	6929	lp12105	2388174	2388623	p	-	unknown	contains an HPT Histidine-containing phosphotransfer (HPT) domain	1.3
3056.1	6928	lp12106	2388928	2395878	p	-	unknown	Similar to polyketide synthase of type I	4.6
2261.1	6863	lp10213	2393330	239494	p	-	unknown	Hypothetical protein	6
3054.1	6927	lp12107	2395875	2397905	p	-	unknown	Similar to two component sensor histidine kinase	1.3
3042.1	6926	lp12114	2414580	2416295	p	-	unknown	Some similarity with eukaryotic proteins	5.2
3417.1	6942	lp10216	242653	243363	p	-	unknown	Similar to ABC-type antimicrobial peptide transport system, ATPase component	1.2
3420.1	6943	lp10217	243357	245723	p	+	unknown	Similar to ABC-type antimicrobial peptide transport system, permease component	1.2
3002.1	6925	lp12148	2454186	2455163	p	+	unknown	Similar to major outer membrane protein	1.1
3422.1	6944	lp10218	245723	246901	p	+	unknown	Similar to membrane protein	1.2
3435.1	6945	lp10226	253065	253781	p	+	unknown	Similar to putative outer membrane protein	1.1
2810.1	6923	lp12284	2603747	2604793	m		unknown	Similar to C-terminal part of transposase	4.5
2809.1	6922	lp12285	2604794	2604934	m	-	unknown	Similar to N-terminal part of transposase	4.5
2808.1	6921	lp12286	2604936	2605313	m	-	unknown	Hypothetical protein	6
2807.1	6920	lp12287	2605322	2605540	m		unknown	Similar to hypothetical protein	6
2806.1	6919	lp12288	2605737	2607245	p	-	unknown	Similar to conserved hypothetical protein	5.2
2805.1	6918	lp12289	2607284	2607952	p	-	unknown		6

2802.1	6917	lpl2291	2608606	2608914	p	-	unknown	Similar to conserved hypothetical protein	5.2
2801.1	6916	lpl2292	2608911	2609849	p	-	unknown	Similar to conserved hypothetical protein	5.2
2798.1	6915	lpl2293	2610374	2611462	m		unknown	Similar to transposase	4.5
2796.1	6914	lpl2294	2611818	2613191	p	-	unknown	Similar to predicted ATPase (AAA+ superfamily)	5.2
2795.1	6913	lpl2295	2613390	2614295	p	-	unknown	Similar to restriction endonuclease	3.2
2782.1	6912	lpl2305	2625469	2626209	p	-	unknown	Similar to acetoacetyl-CoA reductase	2.4
2777.1	6911	lpl2308	2629983	2630168	m	-	unknown	Hypothetical protein	6
2775.1	6910	lpl2309	2630203	2631090	m	-	unknown	Similar to universal stress protein	4.1
2749.1	6909	lpl2323	2647610	2648674	p	-	unknown	Some similarity with eukaryotic proteins	5.2
2738.1	6908	lpl2330	2656109	2657023	p	-	unknown	Some similarity with eukaryotic proteins	5.2
2723.1	6906	lpl2340	2669004	2669732	p	+	unknown		6
2722.1	6905	lpl2341	2669753	2671468	p	-	unknown	Similar to beta-lactamase precursor	4.2
2720.1	6904	lpl2342	2671598	2672392	m	+	unknown		6
2719.1	6902	lpl2343	2672575	2673126	p	-	unknown		6
2717.1	6901	lpl2344	2673318	2675249	m	-	unknown	Ankyrin repeat protein	6
2708.1	6900	lpl2350	2682950	2683255	p		Unknown		6
2706.1	6899	lpl2351	2683321	2683521	p	-	unknown	Hypothetical protein	6
2701.1	6898	lpl2354	2686212	2687375	m	-	unknown		6
2696.1	6896	lpl2358	2689651	2689839	m	-	unknown	Hypothetical protein	6
2660.1	6893	lpl2384	2713562	2715481	m	-	unknown	Some similarity with Legionella effector protein B	5.1
2658.1	6891	lpl2385	2715575	2717098	p	-	unknown	Similar to SidD protein	5.1
2640.1	6890	lpl2399	2729218	2729607	p	-	unknown	Similar to hypothetical protein	5.2
2587.1	6889	lpl2443	2784183	2784362	p	+	Unknown		6

2584.1	6888	lpl2445	2785779	2786138	p	-	unknown	Some similarity with transcriptional regulators	3.5.2
2558.1	6887	lpl2465	2806208	2806354	m	-	unknown	Hypothetical protein	6
2547.1	6886	lpl2472	2811871	2812713	p	-	unknown		6
2541.1	6885	lpl2476	2816937	2818298	m	-	unknown	Similar to protein kinase	3.8
2540.1	6884	lpl2477	2818401	2819000	m	-	unknown	Some similarity with eukaryotic proteins	6
2539.1	6883	lpl2478	2819044	2819529	m	-	unknown	Similar to transposase	4.5
2534.1	6882	lpl2483	2824095	2824961	p	-	unknown		6
2533.1	6881	lpl2484	2824980	2825720	p	-	unknown	Similar to heat shock protein DnaJ	4.1
2532.1	6880	lpl2485	2825862	2826545	p	-	unknown		6
2531.1	6879	lpl2486	2826766	2828007	p	-	unknown	Similar to phage-related integrase	4.4
2530.1	6878	lpl2487	2828021	2829058	p	-	unknown	Similar to putative virulence proteins	5.2
2529.1	6877	lpl2488	2829356	2832133	m	-	unknown	Similar to helicase	3.7.4
2527.1	6876	lpl2489	2832440	2833039	p	-	unknown	Similar to conserved hypothetical protein	5.2
2526.1	6875	lpl2490	2833042	2834082	p	-	unknown	Similar to conserved hypothetical protein	5.2
2525.1	6874	lpl2491	2834127	2834498	p	-	unknown		6
2524.1	6873	lpl2492	2835267	2835971	p	-	unknown	Similar to Legionella LvrA protein	5.1
2523.1	6872	lpl2493	2836365	2839757	p	-	unknown	Similar to conserved hypothetical protein	5.2
2521.1	6871	lpl2494	2839769	2846089	p	-	unknown	Similar to other protein	5.2
2518.1	6870	lpl2495	2846774	2847583	p	-	unknown		6
2517.1	6869	lpl2496	2847573	2848469	p	-	unknown	Similar to integrase	4.5
2516.1	6868	lpl2497	2848638	2849378	m	-	unknown	Similar to hypothetical protein	5.2
2441.1	6867	lpl2545	2905983	2906834	m	+	unknown		6
2440.1	6866	lpl2546	2906910	2908442	m	-	unknown		6
2422.1	6865	lpl2558	2921462	2921779	m	-	unknown	Similar to hypothetical protein	5.2
2392.1	6864	lpl2580	2948197	2948331	m	-	unknown	Hypothetical protein	6
1434.1	6793	lpl2732	3125135	3125284	m	-	unknown	hypothetical gene	6

1422.1	6792	lpl2741	3134300	3136033	m	-	unknown			6
1321.1	6791	lpl2806	3208466	3210055	m	-	unknown			6
3536.1	6946	lpl0286	321867	322067	m	-	unknown		Hypothetical protein	6
3537.1	6947	lpl0287	322127	322402	m	-	unknown		Hypothetical protein	6
1297.1	6790	lpl2826	3226572	3227516	p	-	unknown		Similar to regulatory protein (GGDEF domains)	1.3
1296.1	6789	lpl2827	3227525	3227884	m	-	Unknown			6
1285.1	6788	lpl2833	3233251	3233541	m	-	unknown		Similar to putative transcriptional regulator	3.5.2
1284.1	6787	lpl2834	3233591	3233854	m	-	unknown		Similar to hypothetical protein	5.2
1283.1	6786	lpl2835	3234032	3234310	p	-	unknown		Putative transposase	4.5
1282.1	6785	lpl2836	3234439	3234627	p	-	unknown		Similar to transposase, truncated	4.5
1280.1	6784	lpl2837	3234734	3235702	p	-	unknown		Similar to unknown protein	5.2
1279.1	6783	lpl2838	3235699	3239094	p	-	unknown		Similar to predicted helicase	3.7.4
1278.1	6782	lpl2839	3239087	3240352	p	-	unknown		Similar to conserved hypothetical protein	5.2
1276.1	6781	lpl2840	3240349	3241290	p	-	unknown		Similar to conserved hypothetical protein	5.2
1275.1	6780	lpl2841	3241306	3242331	p	-	unknown		Similar to conserved hypothetical protein	5.2
1274.1	6779	lpl2842	3242341	3242895	p	-	unknown		Similar to conserved hypothetical protein	5.2
1258.1	6776	lpl2843	3247702	3248046	m	-	unknown		Similar to conserved hypothetical protein	5.2
1255.2	6775	lpl2845	3248864	3249910	m	-	unknown		Similar to transposase	4.5
1252.1	6774	lpl2847	3251745	3252164	p	-	unknown		Similar to conserved hypothetical protein	5.2
1251.1	6773	lpl2848	3252157	3252483	p	-	unknown		Similar to hypothetical protein	5.2
1237.2	6770	lpl2857	3261124	3263307	m	-	unknown			6
1221.1	6769	lpl2867	3272087	3272719	p	-	unknown		Similar to hypothetical protein	5.2
1219.1	6768	lpl2868	3273424	3274155	p	-	unknown		Similar to transposase	4.5

1217.1	6767	lpl2869	3274633	3275688	p	-	unknown	Similar to transposase, IS630 family	4.5
1209.1	6766	lpl2875	3281005	3282111	m	+	unknown		6
1207.1	6765	lpl2876	3282392	3283471	p	-	unknown	Similar to ADP-heptose:LPS heptosyltransferase II	1.1
1206.1	6764	lpl2877	3283525	3284478	m		unknown		6
1204.1	6763	lpl2879	3285124	3286263	m		unknown	Similar to O-acyltransferase	1.1
1130.1	6759	lpl2933	3344995	3345129	m	-	rpmH 50S ribosomal protein L34		3.7.1
4085.1	7008	lpl0408	457457	457585	m	+	unknown	putative lipopeptide	1.2
4093.1	7009	lpl0415	460811	460954	p	-	unknown	similar to choline dehydrogenase (N- terminal part)	5.2
4111.1	7010	lpl0432	480791	480895	m	-	Unknown		6
1073.1	6753	lpl0044	50805	51017	m	-	unknown		6
3728.1	6948	lpl0552	600859	601902	p	-	unknown		6
3743.2	6949	lpl0565	609922	612612	m	-	unknown	similar to cation transport ATPase conserved hypothetical protein, some similarity with stress proteins	1.2
3744.1	6950	lpl0566	612655	613590	m	-	unknown	Similar to potassium efflux transporter	5.2
3745.1	6951	lpl0567	613744	615438	p	+	unknown		1.2
1059.1	6751	lpl0057	61500	62498	p	-	unknown		6
3747.2	6952	lpl0568a	615466	616026	m	-	unknown	Similar to C-terminal part of universal stress protein UspA	4.1
3748.2	6953	lpl0568b	616060	616332	m	-	unknown	Similar to N-terminal part of universal stress protein UspA	4.1
3749.2	6954	lpl0569	616397	616690	p	-	unknown	Similar to transposase	4.5
3788.1	6955	lpl0593	643200	643352	m	-	unknown	Hypothetical protein	6
3793.1	6956	lpl0596	644825	645706	m	-	unknown	Similar to aminoglycoside phosphotransferase	4.2
1535.1	6795	lpl0612	665033	666556	p	-	unknown	Similar to UDP-N- acetylglucosamine 1- carboxyvinyltransferase	1.1

1050.1	6750	lp10063	68898	70691	p	-	unknown	Some similarity with eukaryotic protein	6
1049.2	6748	lp10064	70860	72278	p	-	unknown	Similar to transposase	4.5
272.1	6903	lp10065	72587	73840	p	-	unknown	Similar to phage-related integrase	4.4
270.1	6897	lp10066	74228	74809	p	-	unknown	Similar to hypothetical protein	5.2
269.1	6895	lp10067	74915	75700	p	-	unknown	Similar to hypothetical protein	5.2
267.1	6894	lp10068	75697	76572	p	-	unknown	Similar to hypothetical protein	5.2
266.1	6892	lp10069	77003	77278	p	-	unknown		6
1697.1	6800	lp10718	806040	806339	p	-	Unknown		6
1718.1	6801	lp10729	820733	821518	p	+	unknown		6
1824.1	6803	lp10801	907894	908922	p	-	unknown	Similar to transposase	4.5
1825.1	6804	lp10802	908919	909056	m	-	unknown	Similar to transposase, truncated	4.5
1826.1	6805	lp10803	909248	910531	p	+	unknown	Similar to hypothetical protein	5.1
1827.1	6806	lp10804	910565	911593	p	-	unknown	Similar to molybdopterin cofactor synthesis protein A	2.1.1
1828.1	6807	lp10805	912012	912104	p	-	Unknown	Similar to transposase, truncated	4.5
1829.1	6808	lp10806	912186	912323	p	-	unknown	Similar to transposase, truncated	4.5
1834.1	6809	lp10811	916637	918157	p	-	unknown	Similar to hypothetical protein	5.1
3859.1	6975	plp10011	11934	12119	p	-	Unknown	Unknown	6
3861.1	6976	plp10012	12176	12334	p	-	unknown	Weakly similar to carbon storage regulator	6
3862.1	6977	plp10013	12468	13214	p	+	unknown	Similar to E.coli TraT complement resistance protein	4.5
3863.1	6978	plp10014	13334	13621	p	+	unknown		6
3850.1	6974	plp10002	1350	2747	p	-	unknown	Some similarity with eukaryotic proteins	6
3865.1	6979	plp10015	13634	13930	p	-	unknown	Similar to putative conjugative transfer protein TraL	4.5
3866.1	6980	plp10016	13940	14509	p	+	unknown	Similar to putative conjugative transfer protein TraE	4.5

3868.1	6981	plp10017	14502	15218	p	+	unknown	Similar to putative conjugative transfer protein TraK	4.5
3870.1	6982	plp10018	15211	16584	p	+	unknown	Similar to putative conjugative transfer protein TraB	4.5
3871.1	6983	plp10019	16605	16871	p	+	Unknown	Similar to conjugative transfer protein TraV	4.5
3873.1	6984	plp10020	16862	19459	p	-	unknown	weakly similar to conjugative transfer protein TraC	4.5
3874.1	6985	plp10021	19450	19785	p	+	unknown	Weakly similar to TrbI protein	4.5
3875.1	6986	plp10022	19782	20417	p	-	unknown	similar to conjugative transfer protein TraW	4.5
3877.1	6987	plp10023	20407	21390	p	-	unknown	similar to conjugative transfer protein TraU	4.5
3878.1	6988	plp10024	21347	21826	p	+	unknown	similar to conjugative transfer protein TrbC	4.5
3880.1	6989	plp10025	21819	23510	p	+	unknown	Similar to putative conjugative transfer protein TraN	4.5
3881.1	6990	plp10026	23503	24243	p	+	unknown	Similar to conjugative transfer protein TraF	4.5
3882.1	6991	plp10027	24243	24749	p	+	Unknown	Weakly similar to putative conjugative transfer protein TrbB	4.5
3884.1	6992	plp10028	24749	26113	p	+	unknown	Similar to conjugative transfer protein TraH	4.5
3886.2	6993	plp10029	26125	28932	p	-	unknown	Similar to sex pilus assembly and mating pair protein TraG	4.5
3848.2	6973	plp10001	275	1336	p	-	unknown	Similar to chromosome partitioning protein parA	3.4
3888.1	6994	plp10030	28934	29521	p	-	unknown		6
3890.1	6995	plp10031	29613	31448	p	-	unknown	Similar to conjugative transfer protein TraD	4.5

3891.2	6996	plp10032	31463	34411	p	-	unknown	similar to conjugative transfer protein TraI	4.5
3893.1	6997	plp10033	34428	34751	p	-	unknown	Some similarity with eukaryotic proteins	6
3894.1	6998	plp10034	35323	35727	m	-	unknown	Similar to conserved hypothetical protein	5.2
3895.1	6999	plp10035	35724	35921	m	-	unknown	Similar to conserved hypothetical protein	5.2
3896.1	7000	plp10036	36007	36225	m		Unknown		6
3815.2	6957	plp10037	36793	37656	m	-	unknown	Similar to antirestriction protein	3.2
3816.1	6958	plp10038	37966	38127	m	-	unknown	Hypothetical protein	6
3818.1	6959	plp10039	38700	39233	m	-	unknown		6
3820.1	6960	plp10040	39807	40790	p	+	unknown	Similar to hypothetical protein	5.2
3822.1	6961	plp10042	41534	41965	p	-	unknown	Similar to conserved hypothetical protein	5.2
3823.1	6962	plp10043	42194	42760	p	-	unknown	Similar to site-specific recombinases	3.3
3827.1	6963	plp10044	45122	45241	m	-	unknown	Hypothetical protein	6
3828.1	6964	plp10045	45347	45472	m	-	unknown	Hypothetical protein	6
3831.1	6965	plp10046	46027	46149	p	-	unknown	Hypothetical protein	5.2
3835.1	6966	plp10047	46715	47269	m	-	unknown	Similar to conserved hypothetical protein	5.2
3836.1	6967	plp10048	47280	48305	m	-	unknown	Similar to conserved hypothetical protein	5.2
3837.1	6968	plp10049	48321	49262	m	+	unknown	Similar to hypothetical protein	5.2
3839.1	6969	plp10050	49259	50524	m	-	unknown	Similar to conserved hypothetical protein	5.2
3840.1	6970	plp10051	50517	53912	m	-	unknown	Similar to helicases	3.3
3841.1	6971	plp10052	53909	54877	m	-	unknown	Similar to uncharacterized protein predicted to be involved in DNA repair	3.2
3843.1	6972	plp10053	55064	55336	m	-	unknown	Similar to transposase	4.5

CLAIMS

1. An isolated or purified nucleotidic sequence:
 - of *Legionella pneumophila* Paris strain, characterized in that it is selected
5 among the sequences SEQ ID N° 3507 and N° 3508, SEQ ID N° 55 and the sequences
SEQ ID N° 1 to SEQ ID N° 54, and SEQ ID N° 56; or
 - of *Legionella pneumophila* Lens strain, characterized in that it is selected
among the sequences SEQ ID N° 6733 and N° 6734.
2. An isolated or purified nucleotidic sequence:
10 (A) of *Legionella pneumophila* Paris strain, characterized in that it is selected
among:
 - a) a nucleotidic sequence comprising at least one sequence having 80 % identity
with the sequences SEQ ID 3507 and 3508, and SEQ ID N° 1 to SEQ ID N° 56;
 - b) a nucleotidic sequence hybridizing in very stringent conditions with the
15 sequences SEQ ID 3507 and 3508, and SEQ ID N° 1 to SEQ ID N° 56;
 - c) a nucleotidic sequence complementing sequences SEQ ID 3507 and 3508 and
SEQ ID N° 1 to SEQ ID N° 56, or complementing a nucleotidic sequence such as
defined in a), or b), or a corresponding nucleotidic sequence of RNA; and
 - d) a nucleotidic sequence of at least 15 nucleotides of fragment representative of
20 sequences SEQ ID 3507 and 3508, and SEQ ID N° 1 to SEQ ID N° 56, or of fragment
representative of their sequence, or
- (B) of *Legionella pneumophila* Lens strain, characterized in that it is selected
among:
 - a) a nucleotidic sequence comprising at least one sequence having 80 % of
25 identity with the sequences SEQ ID 6733 and 6734;
 - b) a nucleotidic sequence hybridizing in very stringent conditions with the
sequences SEQ ID 6733 and 6734;
 - c) a nucleotidic sequence complementing sequences SEQ ID 6733 and
6734; or complementing a nucleotidic sequence such as defined in a), or b), or a
30 corresponding nucleotidic sequence of RNA; and
 - d) a nucleotidic sequence of at least 15 nucleotides of fragment
representative of sequences SEQ ID 6733 and 6734; or of fragment representative of
their sequence.

3. The nucleotidic sequence as claimed in Claim 2, characterized in that it coded for:

- a polypeptide selected among the polypeptide sequences SEQ ID N° 3509 to SEQ ID N° 6732, and among the polypeptide sequences SEQ ID N° 57 to SEQ ID N° 3455; or

- a polypeptide selected among the polypeptide sequences SEQ ID N° 6735 to SEQ ID N° 7061, specific polypeptide of the Lens strain relative to the Paris strain.

4. A nucleotidic sequence characterized in that it comprises a nucleotidic sequence selected among:

a) a nucleotidic sequence as claimed in Claim 3 or the sequences SEQ ID Nos. 7074 to 7076;

b) a nucleotidic sequence comprising at least 80 % of identity with a nucleotidic sequence as claimed in Claim 3;

c) a nucleotidic sequence hybridizing in very stringent conditions with a nucleotidic sequence as claimed in Claim 3;

d) a complementary nucleotidic sequence or RNA corresponding to a sequence such as defined in a), b) or c); and

e) a nucleotidic sequence of fragment representative of at least 15 nucleotides of a sequence such as defined in a), or d);

5. A polypeptide coded by a nucleotidic sequence as claimed in any one of Claims 2 to 4.

6. The polypeptide as claimed in Claim 5, characterized in that it is selected among the polypeptide sequences:

- SEQ ID N° 3509 to SEQ ID N° 6732, and among the sequences SEQ ID N° 57 to SEQ ID N° 3455; or

- SEQ ID N° 6735 to SEQ ID N° 7061.

7. A polypeptide characterized in that it comprises a polypeptide selected among:

a) a polypeptide as claimed in any one of Claims 5 and 6;

b) a polypeptide having at least 80 % of identity with a polypeptide as claimed in any one of Claims 5 and 6; and

c) a biologically active fragment of at least 5 amino acids of a polypeptide as claimed in any one of Claims 5 and 6.

8. A nucleotidic sequence coding for a polypeptide as claimed in Claim 7.

9. The nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a polypeptide specific to a bacteria of the *Legionella* genre, or one of its fragments of at least 5 amino acids, or its complementary nucleic sequence.

5 10. The nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a polypeptide specific to a pathogenic bacteria of the genre *Legionella* and/or of the *Legionella pneumophila* species, or one of its fragments of at least 5 amino acids, or characterized in that it is a specific repeated sequence of the *Legionella pneumophila* species, in particular the sequence SEQ ID N° 7074, or its
10 complementary nucleic sequence.

11. The nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a specific polypeptide of a bacteria of the *Legionella pneumophila* species Paris strain and/or Lens and/or Philadelphia strains, or one of its fragments of at least 5 amino acids, or its complementary nucleic sequence.

15 12. The nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a specific polypeptide of a bacteria of the *Legionella pneumophila* species Paris strain relative to the Philadelphia strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptide sequences SEQ ID Nos. 3410, 171, 337, 481, 652, 1148, 1521, 2843, 3037, 3181 or one
20 of its fragments of at least 5 amino acids or its complementary nucleic sequence; or

- nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a specific polypeptide of a bacteria of the species *Legionella pneumophila* Paris strain relative to the Lens and Philadelphia strains, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides
25 whereof the sequences are indicated in Table XVII; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

- nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a specific polypeptide of a bacteria of the *Legionella pneumophila* species Lens strain relative to the Paris and Philadelphia strains, or one of
30 its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XVIII; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

- nucleotidic sequence characterized in that it codes for a specific polypeptide of a bacteria of the *Legionella pneumophila* species Philadelphia strain relative to the Lens

and Paris strains, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XI; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

5 - nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a polypeptide present at the same time in the Paris and Lens strain and absent from the Philadelphia strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XIX; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

10 - nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a polypeptide present at the same time in the Paris and Philadelphia strains, and absent from the Lens strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XX; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

15 - nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a polypeptide present at the same time in the Philadelphia strain and Lens, and absent from the Paris strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XXI; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence.

25 13. The nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a surface polypeptide of *Legionella pneumophila* Paris strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptide sequences SEQ ID Nos. 3410, 704, 746, 2267, 2751, 3192, 3218, 3221, 3222, 3317, 3324, 136, 171, 310, 337, 481, 527 652, 664, 893, 972, 1148, 1298, 1361, 1503, 1521, 1576, 1651, 1755, 1847, 1877, 2224, 2406, 2843, 2930, 3037, 3139, 3157, 3165, 3181, or one of its fragments of at least 5 amino acids, or its complementary nucleic sequence.

30 14. The nucleotidic sequence as claimed in Claim 13, characterized in that it codes for a surface polypeptide specific to *Legionella pneumophila* Paris strain relative to the Philadelphia strain, selected among the polypeptide sequences SEQ ID Nos. 3410, 171, 337, 481, 652, 1148, 1521, 2843, 3037, 3181, or one of its fragments of at least 5 amino acids, or its complementary nucleic sequence.

15. The nucleotidic sequence as claimed in any one of Claims 2 to 4, and 8, characterized in that it codes for a polypeptide implied in the polysaccharide biosynthesis of cellular envelope of *Legionella pneumophila* Paris strain, in particular selected among the polypeptide sequences SEQ ID Nos. 1126, 3218, 288, 632, 917,
5 1503, 1555, 1877, 1928, 1963, 2204, 2212, 2243, 2324, 2378, 2410, 2411, or one of its fragments representative of at least 5 amino acids, or its complementary nucleic sequence.

16. The polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a polypeptide specific to a bacteria of the genre *Legionella*, or one of its
10 fragments of at least 5 amino acids.

17. The polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a polypeptide specific to a pathogenic bacteria of the *Legionella* genre and/or of the *Legionella pneumophila* species, or one of its fragments representative of at least 5 amino acids.

18. The polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a specific polypeptide of a bacteria of the *Legionella pneumophila* species Paris strain, or one of its fragments representative of at least 5 amino acids.

19. The polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a specific polypeptide of a bacteria of the *Legionella pneumophila* species Paris strain relative to the Philadelphia strain, or one of its fragments representative of at least 5 amino acids, in particular selected among the polypeptide sequences SEQ ID Nos. 3410, 171, 337, 481, 652, 1148, 1521, 2843, 3037, 3181, or one of its fragments representative of at least 5 amino acids; or

- polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a specific polypeptide of a bacteria of the *Legionella pneumophila* species Paris strain relative to the Lens and Philadelphia strains, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XVII or one of their fragments of at least 5 amino acids; or

- polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a specific polypeptide of a bacteria of the *Legionella pneumophila* species Lens strain relative to the Paris and Philadelphia strains, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XVIII; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

- polypeptide characterized in that it is a specific polypeptide of a bacteria of the *Legionella pneumophila* species Philadelphia strain relative to the Lens and Paris strains, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XI; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

- polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a polypeptide present at the same time in the Paris strain and Lens strain and absent from the Philadelphia strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XIX; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

- polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a polypeptide present at the same time in the Paris and Philadelphia strains, and absent from the Lens strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XX; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence; or

- polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a polypeptide present at the same time in the Philadelphia strain and Lens, and absent from the Paris strain, or one of its fragments of at least 5 amino acids, in particular selected among the polypeptides whereof the sequences are indicated in Table XXI; or one of their fragments of at least 5 amino acids or their complementary nucleic sequence.

20. The polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a surface polypeptide of *Legionella pneumophila* Paris strain, or one of its fragments representative of at least 5 amino acids, in particular selected among the polypeptide sequences SEQ ID Nos. 3410, 704, 746, 2267, 2751, 3192, 3218, 3221, 3222, 3317, 3324, 136, 171, 310, 337, 481, 527 652, 664, 893, 972, 1148, 1298, 1361, 1503, 1521, 1576, 1651, 1755, 1847, 1877, 2224, 2406, 2843, 2930, 3037, 3139, 3157, 3165, 3181, or one of its fragments representative of at least 5 amino acids.

21. The polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a surface polypeptide specific to *Legionella pneumophila* Paris strain relative to the Philadelphia strain, selected among the polypeptide sequences SEQ ID Nos. 3410,

171, 337, 481, 652, 1148, 1521, 2843, 3037, 3181, or one of its fragments representative of at least 5 amino acids.

22. The polypeptide as claimed in any one of Claims 5 to 7, characterized in that it is a polypeptide implied in the biosynthesis of polysaccharide of cellular envelope
5 of *Legionella pneumophila* Paris strain, in particular selected among the polypeptide sequences SEQ ID Nos. 1126, 3218, 288, 632, 917, 1503, 1555, 1877, 1928, 1963, 2204, 2212, 2243, 2324, 2378, 2410, 2411, or one of its fragments representative of at least 5 amino acids.

23. The nucleotidic sequence as claimed in any one of Claims 1 to 4, and 8
10 to 15, and/or polypeptide sequence as claimed in any one of Claims 5 to 7, and, 16 to 22, characterized in that said sequence(s) is (are) registered on a registration support whereof the form and nature facilitate reading, analysis and/or exploitation of said sequences.

24. A registration support, characterized in that it has registered in it a
15 nucleotidic or polypeptide sequence as claimed in Claim 23.

25. Utilization of a support as claimed in Claim 24 for selecting primers or nucleotidic probes for determining the presence of a gene specific to a bacteria of the *Legionella* genre, or specific to a pathogenic bacteria of the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains or specific to a
20 bacteria of the *Legionella pneumophila* species Paris strain and/or Lens and/or Philadelphia strains relative to the Paris strain and/or Lens and/or Philadelphia strains, in a sample.

26. The utilization of a support as claimed in Claim 24 for study of the
25 genetic bacteria polymorphism of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains.

27. The utilization of a support as claimed in Claim 24, for study of other
30 genomes in particular for automatic annotation of genes originating from other genomes.

28. A nucleotidic sequence utilizable as a primer or as probe, characterized in that said sequence is selected among the nucleotidic sequences as claimed in any one of Claims 2 to 4, and, 8 to 15 or among the sequences SEQ ID Nos. 7074 to 7076 or their complementary sequence or their fragment of at least 15 nucleotides.

29. The nucleotidic sequence as claimed in Claim 28, characterized in that it is marked.

30. The nucleotidic sequence as claimed in any one of Claims 28 and 29, characterized in that it is immobilized on a support, covalently or non-covalently.

5 31. The nucleotidic sequence as claimed in Claim 30, characterized in that it is immobilized on a support such as a high-density filter or a DNA chip.

32. The nucleotidic sequence as claimed in any one of Claims 28 to 31 for detection and/or amplification of nucleic sequences.

10 33. A DNA chip or filter, characterized in that it contains at least one nucleotidic sequence as claimed in Claim 32.

34. The DNA chip or filter as claimed in Claim 33, characterized in that it also contains at least one nucleotidic sequence of a microorganism other than *Legionella pneumophila* Paris strain and/or Lens and/or Philadelphia strains immobilized on the support de said chip.

15 35. The DNA chip or filter as claimed in Claim 34, characterized in that the other microorganism is selected from a microorganism of the *Legionella*, genre especially of the *pneumophila* species.

20 36. A kit or necessary for the detection and/or identification of a specific bacteria of the *Legionella* genre, or of a pathogenic bacteria specific to the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain and/or Lens and/or Philadelphia strains, or specific to a bacteria of the *Legionella pneumophila* species Paris strain and/or Lens and/or Philadelphia strains relative to the Paris strain, and/or Lens and/or Philadelphia strains, in a sample, characterized in that it comprises a DNA chip or a filter as claimed
25 in any one of Claims 33 to 35.

30 37. A kit or necessary for the detection and/or quantification of the expression of at least one gene of a specific bacteria of the *Legionella* genre, or of a pathogenic bacteria specific to the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains, or specific to a bacteria of the *Legionella pneumophila* species Paris strain relative to the Paris strain, and/or Lens and/or Philadelphia strains, in a sample, characterized in that it contains a nucleotidic sequence as claimed in any one of Claims 2 to 4 and 8 to 15.

38. A cloning vector, and/or expression vector, characterized in that it contains a nucleotidic sequence as claimed in any one of Claims 2 to 4 and 8 to 15.

39. The cloning vector, and/or expression vector as claimed in Claim 38, characterized in that it contains a nucleotidic sequence as claimed in Claim 13.

5 40. The cloning vector, and/or expression vector as claimed in Claim 38, characterized in that it contains a nucleotidic sequence as claimed in Claim 14.

41. A host cell, characterized in that it is transformed by a vector as claimed in any one of Claims 38 to 40.

10 42. A vegetable or animal, except human, comprising a cell transformed as claimed in Claim 41.

43. A preparation process for a polypeptide, characterized in that a cell transformed by a vector is cultivated as claimed in any one of Claims 38 to 40 in conditions allowing expression of said polypeptide and in that said recombinant polypeptide is recovered.

15 44. A recombinant polypeptide capable of being obtained by a process as claimed in Claim 43.

45. A preparation process for a synthetic polypeptide as claimed in any one of Claims 5 to 7, 16 to 22, characterized in that chemical synthesis of said polypeptide is carried out.

20 46. A hybrid polypeptide, characterized in that it comprises at least the sequence of a polypeptide as claimed in any one of Claims 20 and 21, and a sequence of a polypeptide capable of inducing an immune response in man or animal.

47. A nucleotidic sequence coding for a hybrid polypeptide as claimed in Claim 46.

25 48. A vector, characterized in that it contains a nucleotidic sequence as claimed in Claim 47.

49. A monoclonal or polyclonal antibody, its fragments, or chimeric antibody, characterized in that it is capable of specifically recognizing a polypeptide as claimed in any one of Claims 5 to 7, 16 to 22.

30 50. An antibody as claimed in Claim 49, characterized in that it is a marked antibody.

51. A process for the detection and/or identification of a specific bacteria of the *Legionella* genre, or of a pathogenic bacteria specific of the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella*

pneumophila species Paris strain, and/or Lens and/or Philadelphia strains, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains relative to the Paris strain and/or Lens and/or Philadelphia strains, in a biological sample, characterized in that it comprises the following steps:

5 a) contact by the biological sample with an antibody as claimed in any one of Claims 49 and 50;

 b) revealing the optionally formed antigen-antibody complex.

52. A process for the detection and/or of quantification of the expression of a gene of a specific bacteria of the *Legionella* genre, or of a pathogenic bacteria specific
10 to the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains relative to the Paris strain and/or Lens and/or Philadelphia strains, in a sample, characterized in that a bacteria of the *Legionella* genre is put in contact with an antibody
15 as claimed in Claim 49 or 50 and in that the optionally formed antigen/antibody complex is detected.

53. The kit or necessary for implementing a process as claimed in Claim 51 or 52, characterized in that it comprises the following elements:

 a) an antibody as claimed in any one of Claims 49 and 50;

20 b) optionally, reagents for constitution of the medium prone to immunological reaction;

 c) optionally, the reagents enabling evidence of the antigen-antibody complexes produced by the immunological reaction.

54. The polypeptide as claimed in any one of Claims 5 to 7, 16 to 22, and 44,
25 or antibody as claimed in any one of Claims 49 and 50, characterized in that it is immobilized on a support, especially a protein chip.

55. A protein chip, characterized in that it contains at least one polypeptide as claimed in any one of Claims 5 to 7, 16 to 22, and 44, or at least an antibody as claimed in any one of Claims 49 and 50, immobilized on the support of said chip.

30 56. The protein chip as claimed in Claim 55, characterized in that it also contains at least one microorganism polypeptide other than *Legionella pneumophila* Paris strain and/or Lens and/or Philadelphia strains, or at least an antibody directed against a microorganism compound other than *Legionella pneumophila* Paris strain and/or Lens and/or Philadelphia strains, immobilized on the support of said chip.

57. A kit or necessary for the detection and/or identification of a specific bacteria of the *Legionella* genre, or of a pathogenic bacteria specific to the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains relative to the Paris strain and/or Lens and/or Philadelphia strains, characterized in that it comprises a protein chip as claimed in any one of Claims 55 and 56.

58. A process for detection and/or identification of a specific bacteria or detection and/or identification and/or quantification of the expression of a gene specific to the *Legionella* genre, or of a pathogenic bacteria specific of the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains relative to the Paris strain and/or Lens and/or Philadelphia strains, in a biological sample, characterized in that it uses a nucleotidic sequence as claimed in any one of Claims 1 to 4, 8 to 15, and 28 to 31.

59. A process as claimed in Claim 58, characterized in that it comprises the following steps:

- a) optionally, isolation of the DNA from the biological sample to be analyzed, or obtaining DNAC from the RNA of the biological sample;
- b) amplification of the DNA of the bacterias present in the sample by means of at least one primer, as claimed in any one of Claims 28 and 29;
- c) evidence and/or quantification of the amplification products.

60. The process as claimed in Claim 58, characterized in that it comprises the following steps:

- a) contact by a nucleotidic probe as claimed in any one of Claims 28 to 31, with a biological sample, the nucleic acid contained in the biological sample having, where required, previously been made accessible to hybridization, in conditions enabling hybridization of the nucleic acid probe of a bacteria of the *Legionella* genre optionally present in said sample;
- b) evidence of the hybrid optionally formed between the nucleotidic probe and the nucleic acid of the biological sample.

61. The process as claimed in Claim 58, characterized in that it comprises the following steps:

a) contact by a nucleotidic probe immobilized on a support as claimed in Claim 30 or 31 with a biological sample, the nucleic acid of the sample having, if required, been previously made accessible to hybridization, in conditions enabling hybridization of the probe to the nucleic acid of a bacteria of the *Legionella* genre optionally present in said sample;

b) contact of the hybrid formed between the nucleotidic probe immobilized on a support and the nucleic acid contained in the biological sample, if required after elimination of the nucleic acid of the biological sample not having hybridized with the probe, with a marked nucleotidic probe as claimed in Claim 29;

10 c) evidence of the novel hybrid form in step b).

62. The process as claimed in Claim 61, characterized in that, prior to step a), the DNA of the biological sample or the DNAC obtained optionally by inverse transcription of the RNA of the sample, is amplified by way of at least one primer as claimed in any one of Claims 28 and 29.

15 63. A kit or necessary for the detection and/or identification of a specific bacteria of the *Legionella* genre, or of a pathogenic bacteria specific to the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains relative to the
20 Paris strain and/or Lens and/or Philadelphia strains, in a biological sample, characterized in that it comprises the following elements:

a) a nucleotidic probe as claimed in any one of Claims 28 to 31;

b) optionally, the reagents necessary for implementing a hybridization reaction;

25 c) optionally, at least one primer as claimed in any one of Claims 28 to 29 as well as the reagents necessary for amplification reaction of the DNA.

64. A kit or necessary for the detection and/or identification of a specific bacteria of the *Legionella* genre, or of a pathogenic bacteria specific to the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the
30 *Legionella pneumophila* species Paris strain, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains relative to the Paris strain and/or Lens and/or Philadelphia strains, in a biological sample, characterized in that it comprises the following elements:

a) a nucleotidic probe, known as capture probe, as claimed in Claim 28;

b) an oligonucleotidic probe, known as revelation probe, as claimed in Claim 29;
c) optionally, at least one primer as claimed in any one of Claims 28 and 29 as well as the reagents necessary for amplification reaction of the DNA.

65. A kit or necessary for the detection and/or identification of a specific
5 bacteria of the *Legionella* genre, or of a pathogenic bacteria specific of the *Legionella* genre and/or of the *Legionella pneumophila* species, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, or specific to a bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains relative to the Paris strain and/or Lens and/or Philadelphia strains, in a biological sample,
10 characterized in that it comprises the following elements:

a) at least one primer as claimed in any one of Claims 28 and 29;
b) optionally, the reagents necessary for carrying out amplification reaction of DNA;
c) optionally, a compound enabling the sequence of the amplified fragment,
15 more particularly an oligonucleotidic probe to be verified as claimed in any one of Claims 28 and 29.

66. The process as claimed in Claims 58 to 62, or kit or necessary as claimed in Claims 63 to 65 for the detection and/or identification of a specific bacteria of the *Legionella pneumophila* species Paris strain, and/or Lens and/or Philadelphia strains
20 relative to the Paris strain and/or Lens and/or Philadelphia strains, characterized in that said primer and/or said probe are selected among the nucleotidic sequences as claimed in Claim 14 or 28, in that said polypeptides are selected among the polypeptides as claimed in Claim 21 and in that said antibodies are selected among the antibodies as claimed in any one of Claims 49 and 50 directed against a polypeptide as claimed in
25 Claim 21.

67. A method for selection of a compound capable of inhibiting the expression of genes implied in the polysaccharide biosynthesis of cellular envelope of bacteria of the *Legionella* Paris species strain and/or Lens and/or Philadelphia strains, characterized in that it comprises the following steps:

30 a) contact by said compound with a bacteria of said Paris strain, said bacteria being in conditions and in a medium appropriate to its culture;

b) determination of the capacity of said compound to inhibit expression of the genes coding for the sequence proteins SEQ ID Nos. 1126, 3218, 288, 632, 917, 1503, 1555, 1877, 1928, 1963, 2204, 2212, 2243, 2324, 2378, 2410, 2411 by way of a process

as claimed in Claim 52 in which said antibody is directed specifically against a polypeptide as claimed in Claim 22, or by way of a process as claimed in any one of Claims 58 and 59 in which the probes or primers are specific to a nucleic sequence as claimed in Claim 15.

5 68. A vaccinal or immunogenic composition, characterized in that it comprises one or more polypeptides as claimed in any one of Claims 20 and 21, and/or one or more hybrid polypeptides as claimed in Claim 47.

69. The vaccinal or immunogenic composition, characterized in that it contains a vector as claimed in any one of Claims 39, 40 and 48.

10 70. The utilization of a composition as claimed in Claim 68 or 69, for preparation of a vaccine or immunogen for prevention or treatment of an infection by pathogenic bacteria belonging to the *Legionella* genre, preferably to the *Legionella pneumophila* species, especially Paris strain or Lens or Philadelphia strains, in association with a pharmaceutically acceptable vehicle and, optionally one or more
15 appropriate adjuvants of immunity.

71. A genomic DNA bank of a bacteria of the *Legionella pneumophila* species Paris strain, characterized in that this is the bank deposited with the CNCM on November 19, 2003, under the order number I-3138.

20 72. A genomic DNA bank of a bacteria of the *Legionella pneumophila* species Lens strain, characterized in that this is the bank deposited with the CNCM on September 23, 2004, under the order number I-3306.

73. A vector or host cell, characterized in that this is the vector or the host cell deposited with the CNCM on September 23, 2004, under the order number I-3305.

25 74. The vector or host cell as claimed in Claim 38 or 42, characterized in that this is the vector or the cell deposited with the CNCM on November 19, 2003, under the order number I-3137.

75. A method for isolation of a polynucleotide of interest present in a bacteria of the *Legionella* genre and absent from a bacteria of another genre, or present in a pathogenic bacteria of the *Legionella* genre and absent from a non-pathogenic
30 bacteria of the *Legionella* genre, or again present in a bacteria of the *Legionella pneumophila* species and absent from a bacteria of any other species of the *Legionella* genre, or again present in a bacteria of the *Legionella pneumophila* species Paris strain and/or Lens and/or Philadelphia strains and if required absent from a bacteria of the

Legionella pneumophila species of any other strain, characterized in that it utilizes at least the bank as claimed in Claims 71 and 72.

76. The method as claimed in Claim 75, characterized in that it comprises the following steps:

- 5 a) - isolating at least one polynucleotide contained in a clone of said DNA bank deposited with the CNCM on November 19, 2003, under the order number I-3138; or
 - isolating at least one polynucleotide contained in a clone of said DNA bank deposited with the CNCM on September 23, 2004, under the order number I-3306;
- b) isolating:
 - 10 - at least one genomic polynucleotide or DNAC of a second bacteria of another genre or of the *Legionella* genre, said second bacteria of the *Legionella* genre belonging to a strain different to the Paris strain or, alternatively,
 - at least one polynucleotide contained in a clone of a DNA bank based on a BAC prepared from the genome of a second bacteria of another genre or of the
 - 15 *Legionella* genre, said second bacteria of the *Legionella* genre belonging to a strain different to the Paris strain;
- c) hybridizing the polynucleotide of stage a) to the polynucleotide of stage b);
- d) selecting the polynucleotides of stage a) which have not formed a hybridization complex with the polynucleotides of stage b); and
- 20 e) characterizing the selected polynucleotide.

77. Utilization of the enzymatic polypeptides or precursors of enzymes of sequences SEQ ID Nos. 3675, 4292, 4267 or 6477 or their specific substrate as a target in a process for colorimetric detection of the presence of bacteria of the *Legionella pneumophila* genre, especially of the Paris strain and/or Lens and/or Philadelphia strains, characterized in that the process makes use of at least one of the substrates of these enzymes or in that it makes use of a stage in which the activity of one at least of these enzymes is detected.

78. A process for revealing the presence or the absence of a bacteria of the *Legionella pneumophila* genre, characterized in that it uses a stage in which the presence of the sequence SEQ ID N° 7074 or one of its fragments representative of this *Legionella pneumophila* genre is detected, or characterized in that it uses the couple of primers of sequences SEQ ID N° 7075 and N° 7076, or a couple of primers derived from this set of primers.

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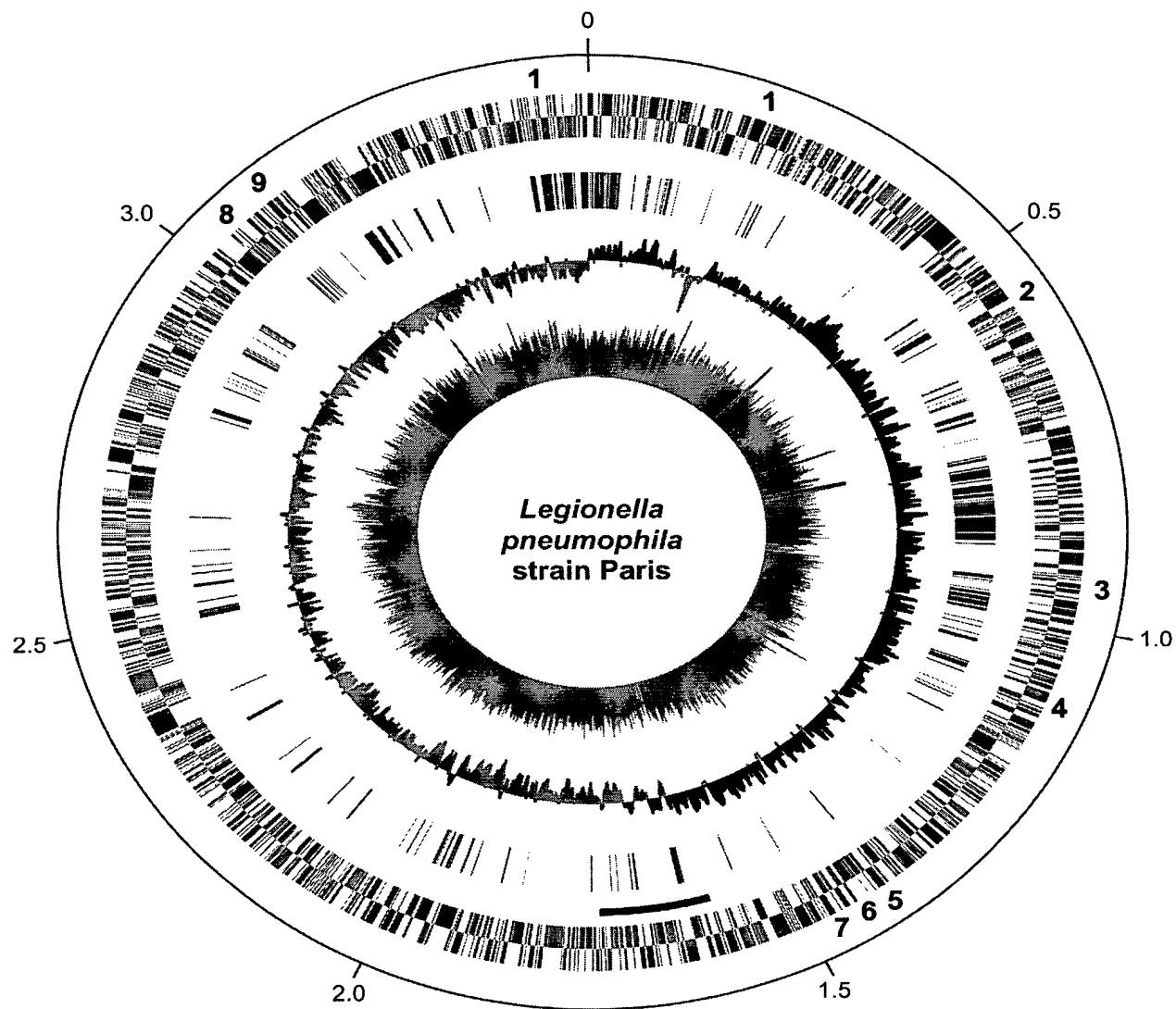


FIGURE 1

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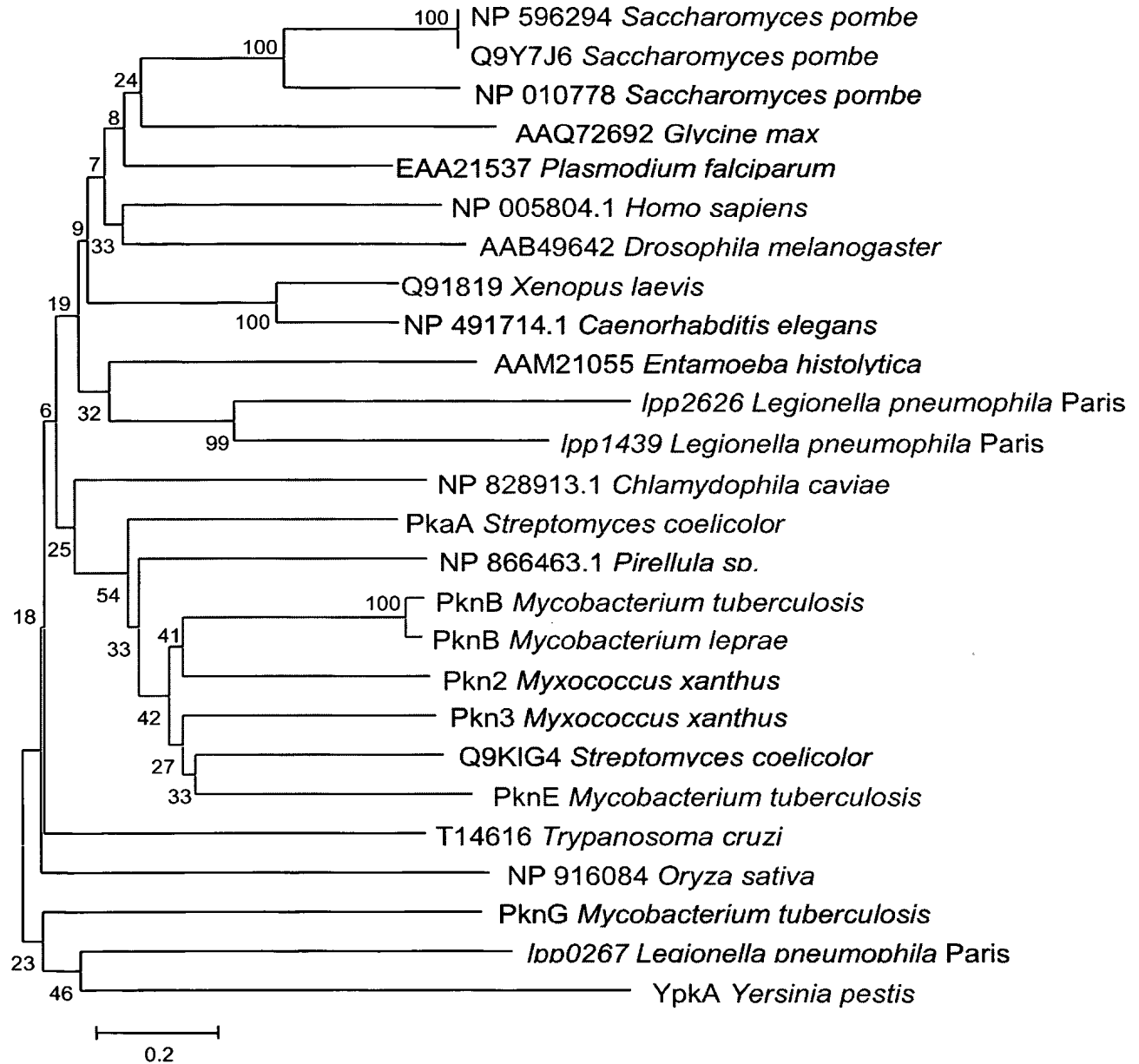
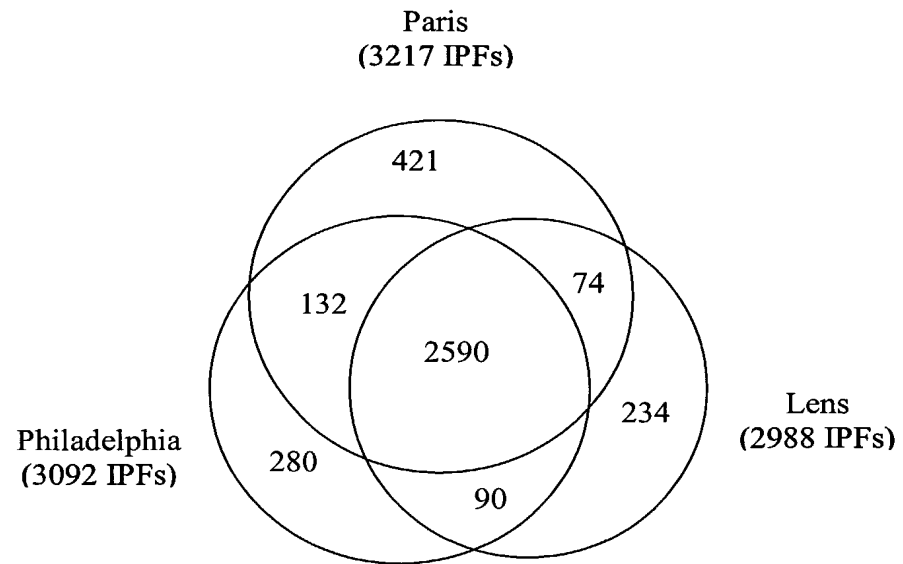
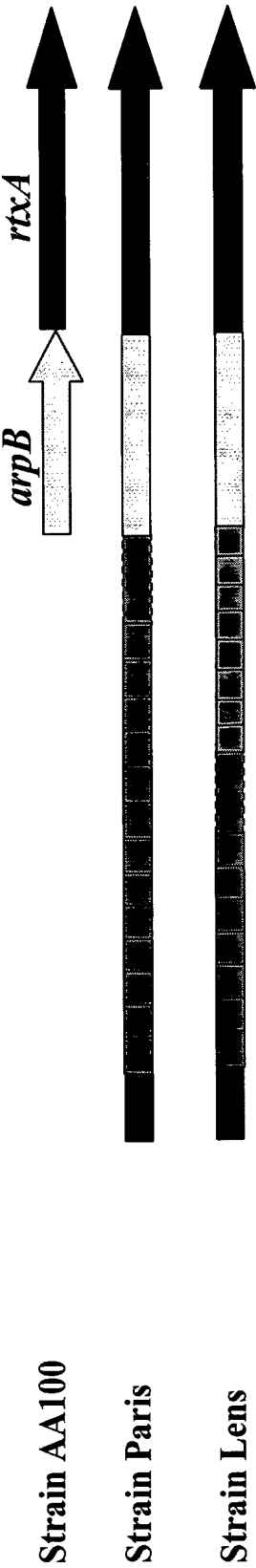


FIGURE 2

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**FIGURE 3**



Strain Paris	...IIFEDDGPVVDMAVKAGAAALTIDETKGVKAGDANANDEAASADANDIGYAKLVGSDLFTLTCKDAGSDGEQS
Strain Lens	...IIFEDDGP SIDGSKVLSADVLTVDETNLGANATASFADNFAQAIDFGE DGAGSVTYAIVLNGSNVGSGLYA TKLTGVVDEDEGLAGGIAGGTGDVAGQAVAAAGNVATL FQSGADAPLSYSLNPNTSGLPAL
Strain Paris	TLFKLLVSAPASGLVD TATNQAIIVLSANAGCTEVLGKNTNGDVVKVLLTASDGDVEVFQYRAIKHENASDH
Strain Lens	IDNLDVSTADGDGIGRGGEIVLNQNGNVVTGSLGGVDYFTITIDEASGEVVFQELASVWHANTANPDDQSAL SSGGVALTYAVSSGGTLTASAGSTQVFTFLNANGNYTFTLLAKLDHPAGADENDITINLGSVIRATDSGDGT
Strain Paris	DESGAGGIIERIQA GSLKLEVTLTDKDGS AKGELDLGQMRFEDDGPVVD
Strain Lens	QALANSLVVRATVVDADGDQAVHDL DV SQGVFQVKDDGPSID VVAAADGLVITVDDDDTPVAST

FIGURE 4

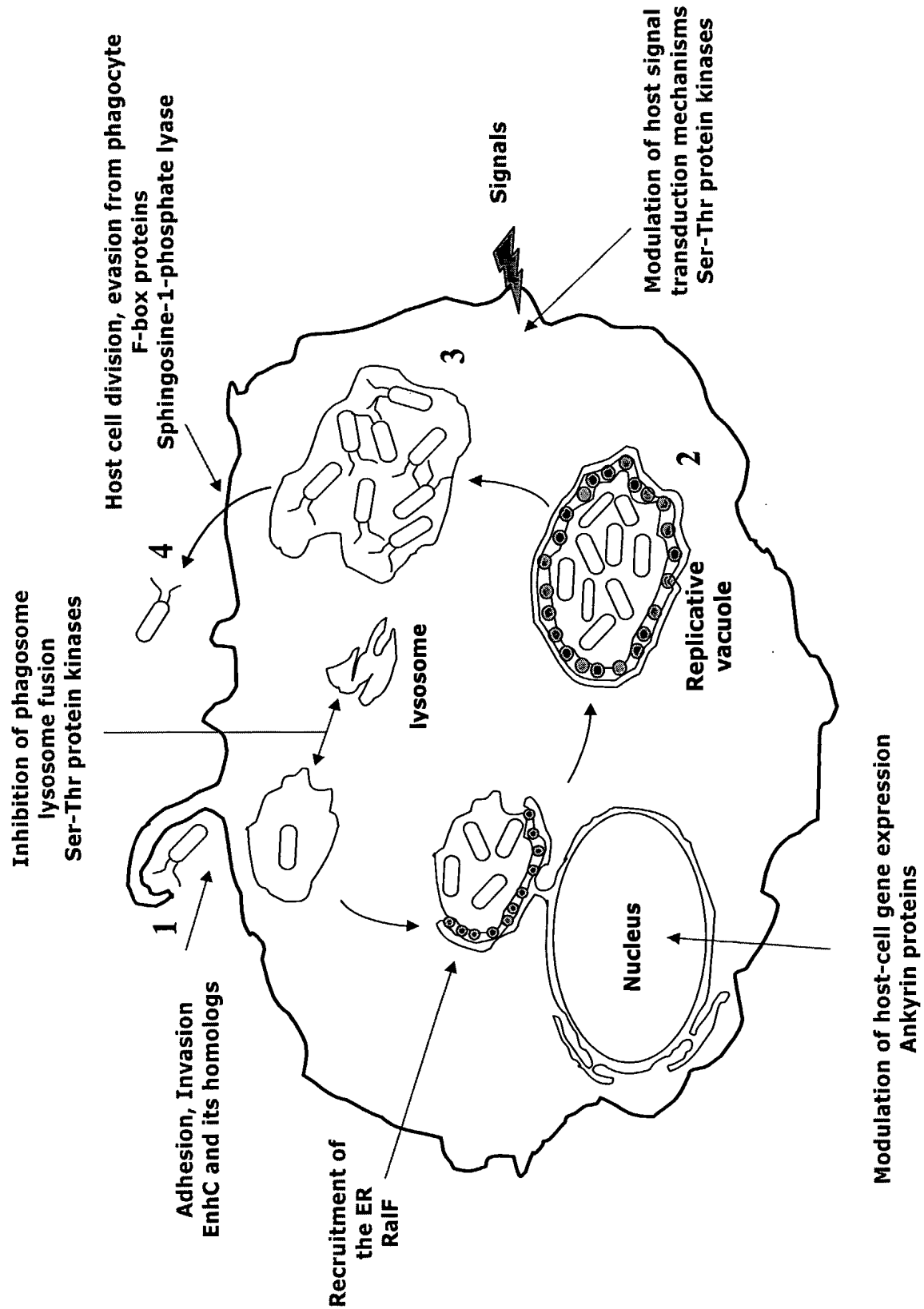


FIGURE 5

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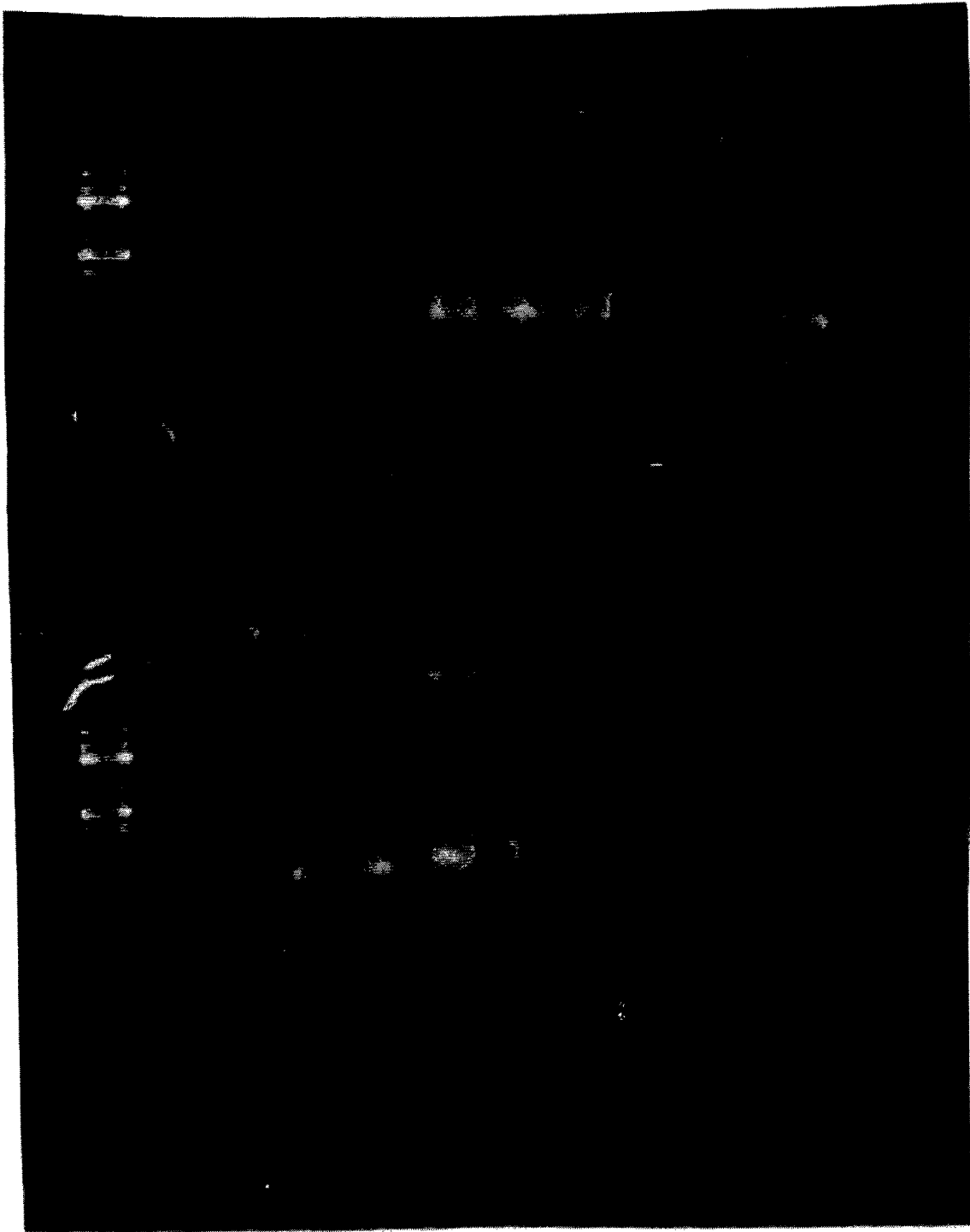


FIGURE 6

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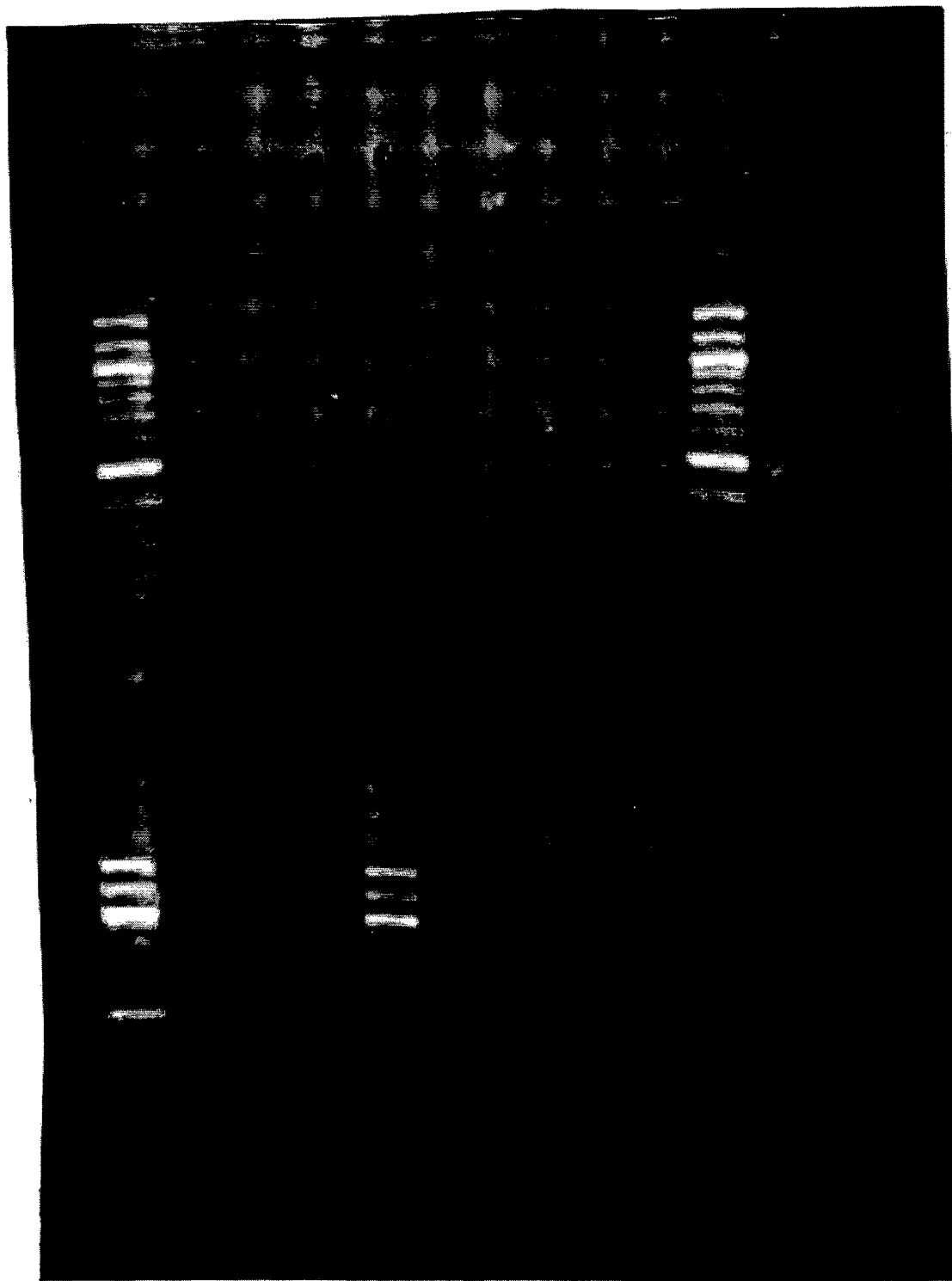


FIGURE 7

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
2 June 2005 (02.06.2005)

PCT

(10) International Publication Number
WO 2005/049642 A3

(51) International Patent Classification:
C07K 14/195 (2006.01) A61K 39/00 (2006.01)

(21) International Application Number:
PCT/IB2004/003578

(22) International Filing Date:
23 September 2004 (23.09.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03/13687 21 November 2003 (21.11.2003) FR

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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv))

Published:

— with international search report
— with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(88) Date of publication of the international search report:

1 June 2006

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: GENOME OF *LEGIONELLA PNEUMOPHILA* PARIS AND LENS STRAIN-DIAGNOSTIC AND EPIDEMIOLOGICAL APPLICATIONS

(57) Abstract: The object of the invention is the genomic sequence and nucleotidic sequences coding for polypeptides of *Legionella pneumophila* Paris strain and Lens strain, such as cellular surface polypeptides, especially specific between these two strains and/or relative to the Philadelphia strain, or implied in the virulence or in the polysaccharide biosynthesis of cellular envelope, as well as vectors including said sequences and cells transformed by these vectors. The invention also concerns processes for detection of these nucleic acids or polypeptides and diagnostic typing kits for bacteria of the *Legionella* genre, especially of the *Legionella pneumophila* species, such as the Paris and Lens strains, between them and/or relative to the Philadelphia strain. The invention especially concerns a repeated nucleic sequence specific to the *Legionella pneumophila* species and its utilization as an analysis target in processes for detection of the presence of these bacteria. The aim of the invention is also a method for selection of compounds capable of modulating the biosynthesis of these polysaccharides of cellular envelope utilizing said nucleotidic sequences or said polypeptides. The invention finally comprises pharmaceutical compositions, especially vaccinal, for the prevention and/or treatment of bacterial infections, in particular by *Legionella pneumophila* Paris strain and/or Lens strain.



WO 2005/049642 A3

INTERNATIONAL SEARCH REPORT

National Application No.

PCT/IB2004/003578

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C07K14/195 C12N15/31 C12Q1/68 G01N33/68 G01N33/569
A61K39/02 A61K48/00 C12N1/21

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, BIOSIS, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5 935 782 A (NICHOLAS P. CIANCIOOTTO ET AL.) 10 August 1999 (1999-08-10) column 3, line 65 - column 4, line 15 column 7, line 23 - column 10, line 9 -----	1-8, 23-66, 68-70
A	HELENA AURELL ET AL.: "Legionella pneumophila Serogroup 1 strain Paris: Endemic distribution throughout France" JOURNAL OF CLINICAL MICROBIOLOGY, vol. 41, no. 7, July 2003 (2003-07), pages 3320-3322, XP002293914 cited in the application the whole document ----- -/--	1-8, 23-66, 68-70



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

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O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

G document member of the same patent family

Date of the actual completion of the international search

6 September 2005

Date of mailing of the international search report

14 09. 2005

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INTERNATIONAL SEARCH REPORT

national Application No

T/IB2004/003578

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE TREMBL 1 October 2002 (2002-10-01), DA SILVA, A.C.R. ET AL.: "3-hydroxybutyryl-CoA dehydratase" XP002329650 Database accession no. Q8PAFO_XANCP the whole document & DA SILVA, A.C.R. ET AL.: "Comparison of the genome of two Xanthomonas pathogens with differing host specificities" NATURE, vol. 417, 2002, pages 459-463, -----</p>	1-8, 23-66, 68-70
A	<p>EP 1 219 628 A (BIOSYNTH AG) 3 July 2002 (2002-07-03) page 2, paragraph 2 - paragraph 3 page 3, paragraph 14 page 3, paragraph 16 - page 4, paragraph 26 -----</p>	77
A	<p>US 5 491 225 A (TERESA K.H. PICONE) 13 February 1996 (1996-02-13) the whole document -----</p>	78

INTERNATIONAL SEARCH REPORT

international application No.
PCT/IB2004/003578

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-8, 23-66, 68-70, 77, 78
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: partially 1-8, 23-66, 68-70

Legionella pneumophila Paris strain polypeptide of sequence SEQ ID NO:3509, nucleotide sequence encoding it and homologues and fragments thereof as well as their uses

2. claims: 9, 16 and partially 23-66, 68-70

Polypeptide specific to a Legionella bacteria or fragment of at least 5 amino acids, nucleotide sequence encoding the same as well as their uses

3. claims: 10, 17, 78 and partially 23-66, 68-70

Polypeptide specific to a pathogenic Legionella bacteria or Legionella pneumophila and fragment thereof of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

4. claims: 11, 18 and partially 23-66, 68-70

Polypeptide specific of a Legionella pneumophila and/or Lens and/or Philadelphia bacteria strains or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

5. claims: partially 12, 19 and partially 23-66, 68-70

Polypeptide specific to a Legionella pneumophila Paris strain relative to the Philadelphia strain or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

6. claims: partially 12, 19 and partially 23-66, 68-70

Polypeptide specific to a Legionella pneumophila Paris strain relative to the Lens and Philadelphia strains or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

7. claims: partially 12, 19 and partially 23-66, 68-70

Polypeptide specific to a Legionella pneumophila Lens strain relative to the Paris and Philadelphia strains or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

8. claims: partially 12, 19 and partially 23-66, 68-70

Polypeptide specific to a Legionella pneumophila Philadelphia strain relative to the Lens and Paris strains or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

9. claims: partially 12, 19 and partially 23-66, 68-70

Legionella polypeptide present at the same time in the Paris and Lens strains and absent in the Philadelphia strain or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

10. claims: partially 12, 19 and partially 23-66, 68-70

Legionella polypeptide present at the same time in the Paris and Philadelphia strains and absent in the Lens strain or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

11. claims: partially 12, 19 and partially 23-66, 68-70

Legionella polypeptide present at the same time in the Philadelphia and Lens strains and absent in the Paris strain or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

12. claims: 13, 14, 20, 21 and partially 23-66, 68-70

Legionella pneumophila Paris strain surface polypeptide or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

13. claims: 15, 22, 67 and 23-66, 68-70

Legionella pneumophila Paris strain polypeptide implied in the polysaccharide biosynthesis of the cellular envelope or fragment of at least 5 amino acids, nucleotide sequence encoding the same, as well as their uses

14. claims: partially 1-8, 23-66, 68-70

Legionella pneumophila Paris strain polypeptide and encoding polynucleotide other than specified above

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

15. claims: partially 1-8, 23-66, 68-70

Legionella pneumophila Lens strain polypeptide and encoding polynucleotide other than specified above

16. claims: 71, 74 and partially 75, 76

Genomic DNA bank of Legionella pneumophila Paris strain I-3138 and vector or host cell comprising the whole genome I-3137 and uses thereof

17. claims: 72, 73 and partially 75, 76

Genomic DNA bank of Legionella pneumophila Lens strain I-3306 and vector or host cell comprising the whole genome I-3305 and uses thereof

18. claim: 77

Use of enzymatic polypeptides of sequences SEQ ID Nos. 3675, 4292, 4267 or 6477 or their substrates for detection of Legionella pneumophila bacteria

19. claim: 78

Use or sequences SEQ ID NOs:7074, 7075 or 7076 for revealing the presence of Legionella pneumophila

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB2004/003578

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
US 5935782	A	10-08-1999	NONE	
EP 1219628	A	03-07-2002	EP 1219628 A1	03-07-2002
			AT 236176 T	15-04-2003
			CA 2430488 A1	04-07-2002
			DE 60001979 D1	08-05-2003
			DE 60001979 T2	19-08-2004
			WO 02051853 A1	04-07-2002
			JP 2004524290 T	12-08-2004
			US 2002151725 A1	17-10-2002
US 5491225	A	13-02-1996	WO 9211273 A1	09-07-1992
			US 5614388 A	25-03-1997
			AU 657286 B2	09-03-1995
			CA 2075493 A1	21-06-1992
			EP 0533854 A1	31-03-1993
			JP 5507206 T	21-10-1993